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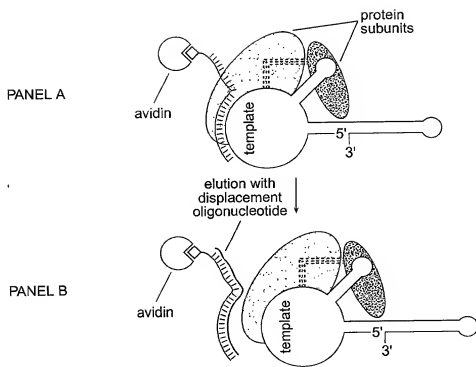


FIG. 1

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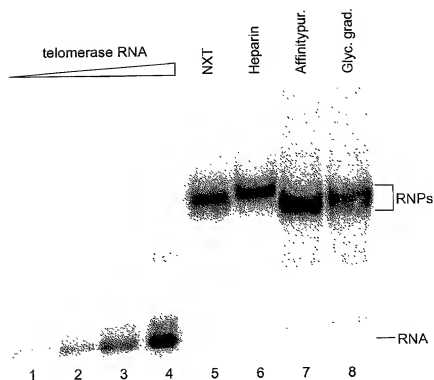


FIG. 2

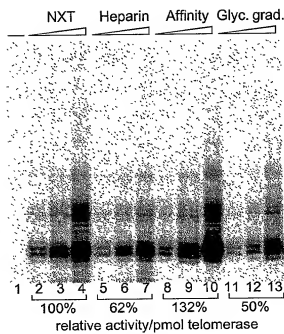


FIG. 3

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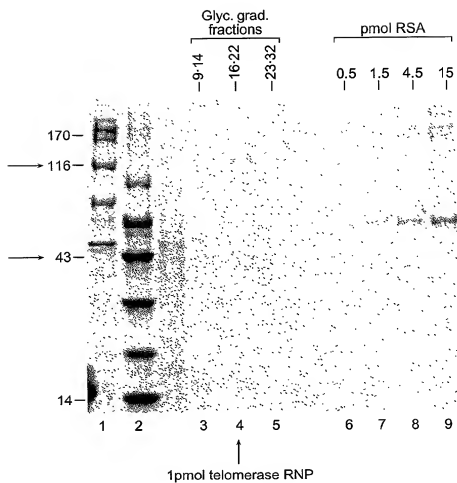


FIG. 4

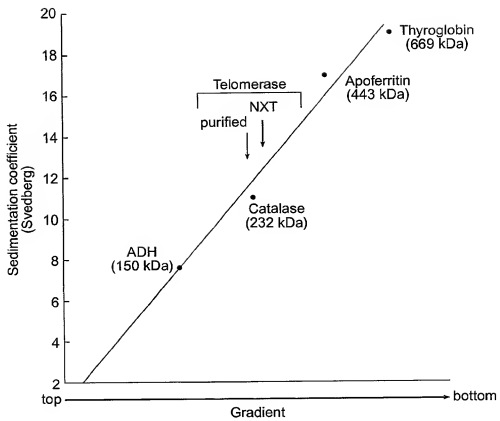


FIG. 5

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Telomerase:

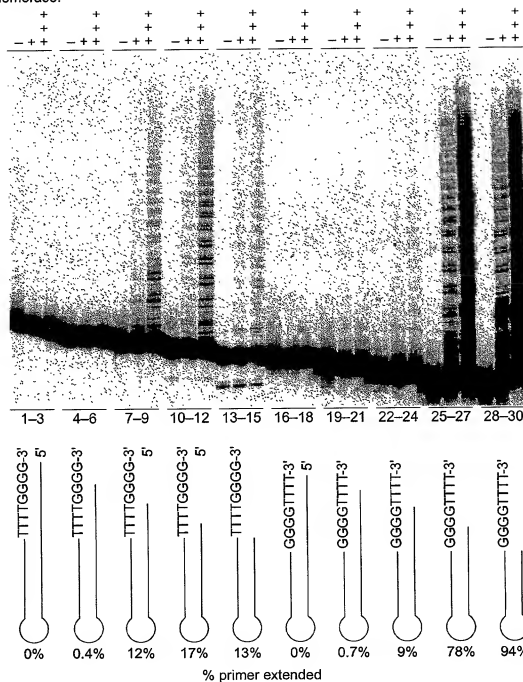


FIG. 6

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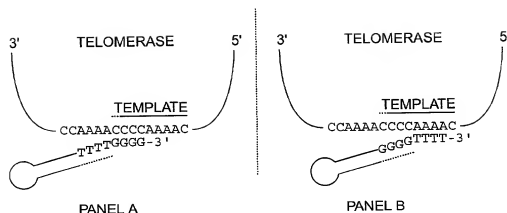


FIG. 7

1	CCCCAARACC	CCAAAACCCC	AAAACCCCTA	TAAAAAAGA	AAAAATTGAG
51	GTAGTTTAGA	AATAAAATAT	TATCCCGCA	CAATGGAGA	TGGATTATGA
101	TTTGGATGAT	ATAGAAAAAT	TACTTCCCTAA	TACATTCAC	AAGTATAGCA
151	GCTCTGTAG	TGACAAGAAA	GGATGCAAAA	CATTGAAATC	TGGCTCGAAA
201	TGCGCTTCAT	TGACTATTCC	AAAGTTGCA	AAACAATTAG	AGTCTACTT
251	CTCGGATGCA	AATCTTTATA	ACGATCTTT	CTTGAGAAA	TTAGTTTAA
301	AAGCGGAGA	GCAAGAGTA	GAAATTGA	CATTACTAAT	GTTTAAATAA
351	AATCAGGTAA	TGAGGATTAT	TCTATTTTT	AGATCACTTC	TTAAGGAGCA
401	TTATGGAGAA	AATTAATTAA	TACTAAAGG	TAAACAGITT	GGATTATTTT
451	CCTAGCCAA	AATGATGAT	ATATTAAAT	CATATGAGAA	TGAGTCAAA
501	GATCTCGATA	CATCAGACT	ACCAAGACA	AACCTGCTAT	AAAACGCAAG
551	AAAAAGTTTG	ATAATCGAAC	AGCAGAAGAA	CTTATTGCAT	TTACIAITCG
601	TATGGGTTTT	ATTACAATTG	TTTTAGGTAT	CGACGGTGAA	CTCCCGAGTC
651	TTGAGACAAT	TGAAAAAGCT	GTTTACAAC	GAAGGAATCG	CAGTTCTGAA
701	AGTTCTGATG	TGATGCGCAT	TATTTTGTA	ATTAACTCA	AATATCTTAT
751	CTCAATTAA	TGATATGCTA	TAGAAACAAA	CCAAATAAAC	CATGCAAGTT
801	TAATGGAATA	TACGTTAAAT	CCTTTGGGAC	AAATGCACAC	TGAATTTATA
851	TTGGATTCTT	AAAGCATAGA	TACACAGAAT	GCTTTAGAGT	CTGATTTAGC
901	TTACAACAGA	TTACCTGTTT	TGATTACTCT	TGCTCATCTC	TTATATCTTT
951	AAAGAAGCA	GCGGAAATGA	AAAGAAGACT	AAAGAAAGAG	ATTTCAAAT
1001	TTGTGTGATC	TTCTGTAACC	GGAATTAACA	ACAAGAATAT	TAGCAACGAA
1051	AAAGAAGAG	AGCTATCAC	ATCCTGATTC	TAAAGATTT	CAAAATTTCC
1101	AGGTAAGAGA	GATACATTC	TAAAAATTC	TATATATAG	TTTTTCAATT
1151	CACAGCTGTT	ATTTCTTTT	ATCTTAACA	TATTTTGTGA	TTTACTGAAA
1201	GTAAGAAGTA	TCAAATAGA	GAGCGCTAG	ACTGAGGTAA	CTTAGCTTTAT
1251	TCAATTCAT	AGATCGACCT	TATATATCC	AATACGATGA	TAAAGAAACA
1301	CGAGTCATCC	GTTTTAAAAA	TAGTGCTATG	AGGACTAAAT	TTTTTAGATC
1351	AGAAATGGA	GCGGAATCT	TAATCAAAAA	GAATTGCGTC	GATATTGCAA
1401	AGAATCGAA	CTCTAAATCT	TTCGTTAATA	AGTATTACCA	ATCTIGATTG
1451	ATTGAAGAGA	TTGACGAGGC	AACGTCACAG	AGATCATTAT	AGAAATTAAT
1501	GTAACCTTTA	TTAATTAGAG	AATAAATAA	ATTACTATAT	TAGAGCTAG
1551	CGATCTTCAA	TTGACGAAAT	AAAGCTGAA	CTAAAGTTAG	ACATTAATAA
1601	ATACAAACCT	TGTCAAAT	ATTGAGGAG	GAAAGAAGA	CCAGTTAGCA
1651	AAAGAAATA	TAGGCAATA	AATAAATGA	GTACAGAAGT	GAGAAATAA
1701	AGAGTTTAT	TTTTTCAATA	ATTATTGAA	AAAGGGGTT	TTGGGGTTTT
1751	GGGTTTTTGG	GG			

FIG. 11

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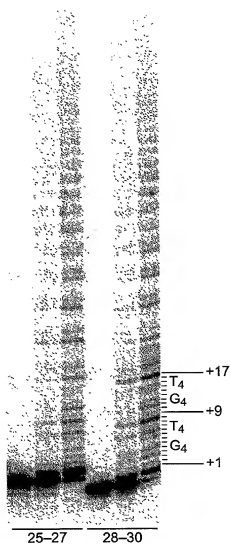


FIG. 8

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1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTTAATTA CAAAACCTAA
 101 ATCGAGGTTG ATGTTTGATA TCAAGCTGAT AATCATGGCA TTCCTCAGC
 151 TCCTTAAGACT TGTGAGAGAA TTAAGAGAC TAAACGTTG TACTCTTGGG
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATTAAGAT
 251 TTAGAAGATA TTAATAATTT TCGCGAGACA AATATTGTTG CTACTCCAGC
 301 AGACTATAAT GAAGAAGATT TTAAGTTTAT TGCAAGAAAA GAAGTATTTT
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTCCA
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAAAC GCTCTTCAA
 501 CTCAAAGCA GTATTCTCTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551 ATTGGAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
 601 GCGAATCTT GAGGGAACCTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651 ATCATTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAAT ACAATGTCAA
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCGG AATTGGAATA
 801 ATATGAAATC AAGAACCCGA ATATTTTATT GCACCTATTT TAATAGAAAT
 851 AACCATTCTC TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951 GAATTAGAAA GAAGCTAATA GATAAGGTTA TCGAAAAAAT TGCCCTACATG
 1001 CTTGAGAAAG TCAAAAGATT TAACCTCAAC TACTATTTAA CAAAATCTTG
 1051 TCCTCTTCCA GAAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACTTGA
 1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACATGAAGA GCTGTTTAGC
 1151 TACACAACTG ATAATAAATG OGTCACACAA TTTATTAATG AATTTTTCTA
 1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
 1251 AAAAGAAAGT TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC
 1301 AAAAATCTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
 1351 GGGTTGAGAC TCTGCAAGAC ATTTTATTA TTTTGATCAC GAAAAATCT
 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGCTCG
 1451 CTGATTAGAT GATTTTTCTA TGTCAACGAG CAACAGAAAAA GTTACTCCAA
 1501 AACCTATTAC TACAGAAAGA ATATTTTGGA CGTCATTATG AAAATGTCAA
 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
 1601 GAAGAATGGA AAAAGTCGCT TGGATTGCA CTTGGAAATC TCAGACTAAT
 1651 ACCGAAGAAA ACTACTTTCC GTCCAAATAT GACTTTCAAT AAGAAGATTG
 1701 TAAATTTCGA CCGGAAGACT ACAAAATTA CTACAAATAC GAAGTTATTG
 1751 AACTCTCACT TAATGCTTTAA GACATTGAAG AATAGAATGT TTAAGATTC
 1801 TTTTGATTTC GCTGTTTTTA ACTATGATGA TGTAAATGAA AAGTATGAGG
 1851 AGTTTGTGTT CAAATGGAAG CAAGTTGGAC AACCAAACT CTTCTTCCA
 1901 ACTATTGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAATCTC
 1951 AACATTCCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
 2001 CTGCACAAAT TCTAAAGAGA AAGAAATGAA AGATTAATTT AGACAGAAAT TCCAGAAGAT
 2051 TTTAGAAAGA AAGAAATGAA ATCCAACTTT ATTCAGTGTG TCTGAAATG
 2101 TGCAATTCGA GGAAGATGAA AGATAACAT TAATTGTTGA AGCAAGCAA
 2151 AGAAATTAAT TTAAGAAGAA TAACTACTTT CAACCAGTCA TTAATATTG
 2201 CCAATATAAT TACATTAAC TTAATGGGAA GTTTTATAAA CAAACCAAAG
 2251 GAATTCCTCA AGGTCCTTGA GTTTCATCAA TTTTGTATC ATTTTATATG
 2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA

FIG. 9

2401 CCCTGAAAAT CCAAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
 2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
 2501 ATAAACGTAA GCTGCTGAAAA TGGATTTTAA TTCAATATGA AGAAACTACA
 2551 GACTAGTTTT CCATTAAAGTC CAAGCAAAAT TGCAAAATAC GGAATGGATA
 2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
 2651 TCAATTGATA TGAAAACCTC TGCTTTAATG CCAAATATTA ACTTGAGAAT
 2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAAACA AAGAAAGCAT
 2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
 2801 CATTATTTTA GAAAGACGAT TACAACCCGA GACTTTGCGA ATAAAACTCT
 2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
 2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
 2951 TTAGAGGTAT CTAAAAATT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
 3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
 3051 ACTTTTTCTC TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
 3101 AAGTACATT TCAACAGAGT TTGCATGATC CTCAAGGCCA AAGAAGCAAA
 3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
 3201 CTATTCTAAC TTATTTTGGG AAGTTAAATT TCAAATTTTG TCTTATATAC
 3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

FIG. 9
(CONTINUED)

1 MEVDVDNQAD NHGHSALKT CERIKEAKTL YSWIQKVIRC RNQSQSHYKD
 51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
 101 SSSDVSDRQK LQCFGQLRG NQLAKTHLLT ALSTQKQYFF QDEWQVVRAM
 151 IGNLFRLHLY TKYLIFQRTS EGTLVQFCGN NVEDHLKVND KFDKKQKGGG
 201 ADMNEPRCS TCKYNVKNK DHFLNNINVP NWNNMKSRTT IPYCTHPNRN
 251 NQPFKHEFV SNKNINISAMD RAQTIPTNIF RPNRIRKKLK DSVIEKIAYM
 301 LEKVDFNFEN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYVEELFS
 351 YTDNKNKVQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHLEIH
 401 KNLLLEKINT REISWMQVET SAKHFYYPFH ENIYVLWLL RNIFEDLVVS
 451 LIRCFYFVTE QOKSYSKTY YRKNINDVIM KMSIADLKE TLAEVQKEV
 501 EEWKKS LGFA PGKLR LIPKK TFRPMTFNN KKVNSDRKT TKLTNTNTKLL
 551 NSHMLMLKTL NRMFKDPFGF AVFNVDVVMK KYEEFVCKWK QVGQPKLFFA
 601 TMDIEKCYDS VNREKLSFTL KTKKLLSDF WIMTAQILKR KNNIVDSKN
 651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLLIVEAKQ
 701 RNYFKDNL L QPVINICQYN YINFNGKPHY QTKGIPQGLC VSSILSSFFY
 751 ATLESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIKEL
 801 INVRENGFK FNMKKLQTSF PLSPSKFAKY GMDSEVEQNI VQDYCDWIGI
 851 SIDMKTLALM PNINLRIEGL LCTLNLMQOT KKASMWLKKK LKSFLMNNIT
 901 HYFRKTIITE DFANKTLNKL FISGGYKYM CAKEYKDHFK KNLAMSSMID
 951 LEVSKI IYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
 1001 KYIFNRVCM LKAKEAKLKS DQCQS LIQVD A

FIG. 10

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FIG. 12

FIG. 12
(CONTINUED)

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FIG. 12
(CONTINUED)

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1381 GAATTGCGTCGATATTGCAAAAGAAATGCAACTCTTAAATCTTTTCGTTAATAGATTATACCA
CTTAAACGCAGCTATAACGTTTCTTCTAGCTTGAAGATTAGAAAGCAATATTATTATTAATGGT 1440

a E L R R Y C K R I E L * I F R * * V L Y P -
b N C V D I A K E S N S K S F V N K Y Y Q -
c I A S I L Q K N R T L N L S L I S I T N -

1441 ATCTTGATTGATTGGAAGAGATTGACGAGGCAACTGCACAGAGATCATTTAAGATAATAAA
TAGAATACTAACTCTCTCTAACTGCTCGTTGACGTGTCTTCTAGTAATTTCTTTATT 1500

a I L I D C R D * R G N C T E D H * R N K -
b S * L I E E I D E A T A Q K I I K E I K -
c * D * L K R L T R Q L H R R S L K K * S -

1501 GTAACCTTTTATTAATTAGAGAATAAATCTAAATCTACTAATATAGAGATCAGCGATCTTCAA
CATTTGAAATAATTAATCTCTTATTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT 1560

a V T F I N * R I N * I T N I E I S D L Q -
b * L L L I R E * T K L L I * R S A I F N -
c N F Y * L E N K L N Y * Y R D Q C R S I -

1561 TTGACGAATAAAGCTGAACCTAAAGTTAGACAACTAAAAATACAAACCTTGGTCAAAT
AACTGCTTTATTTTGACTTGATTCAATCTGTATTTTTTATGTTTGGAACCAAGTTTTA 1620

a L T K * K L N * S V R * T I K N T N L G Q N -
b * R N K S * T K V R Q * K I Q T L V K I -
c D E I K A E L K L D N K K Y K P W S K Y -

1621 ATTGAGGAAGGAAGAAGACCCAGTTAGCAAAAGAAAAAATAGGCAATAAATAAATGA
TAACCTCCTCCTTTTCTCTGGTCAATCGTTTCTTTTATTCCGTTATTATTTTACT 1680

a I E R E G K E D Q L A K E K K I R N * I K * -
b L R K E K K K T S * Q K K K * G N K * N E -
c * G R K R R P V S K R K N K A I N K M S -

1681 GTACGAGGTGGAAGAAATAAAGATTATTTTTTCAATAATTTATTGAAAAGAGGGGTT
CATGCTTCCACTCTTATTTTCTAAATAAAAAAGTATTAAATAACTTTTCTCCCA 1740

a V Q K * R N K R D I F F F N N L L K R G V -
b Y R S E E I K R D L F F S I I Y * K E G V -
c T E V K K * K I Y F F F Q * F I E K R G F -

1741 TTGGGGTTTGGGGTTTGGGG
AACCOCAAAACCCCAAAACCCC 1762

a L G F W G F G -
b W G F G V L G -
c G V L G F W -

FIG. 12
(CONTINUED)

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2 EVDVQONQADNHGIHSALKTCETKEAKTLYSWIQKVIRCRNQSQSHYKDL 51
| : : : | : : : | : : : | : : : | : : : |
19 ELELEMQENQNDIQVRVK...IDDPKQY..LVNVTAACLLQEGSVYQDK 62
| : : : | : : : | : : : | : : : | : : : |
52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF..STOLMIELIDKCLVELL 100
| : : : | : : : | : : : | : : : | : : : |
63 DERRYIITKALL...EVAESDPPEFIQCLAVYIRNELYIRTTTNYIVAF. 107
| : : : | : : : | : : : | : : : | : : : |
201 SSSDVSDRQKLQCPGFQKGNQALKTLLTALSTQKQYFFQDEWNOVRAM 150
| : : : | : : : | : : : | : : : | : : : |
208 .....CVVHKNTQPFIEKYPNKAVLLPNDLLEVCEFAQVLYI 144
| : : : | : : : | : : : | : : : | : : : |
2151 IGNELFRHLYTKYLIFORTSEBTLVQFCGNNVFDHLKVNDKPKKQKGGGA 200
| : : : | : : : | : : : | : : : | : : : |
2145 FDATEFKNLY.....LDRILSQDIRKELTFRKCLQRCVRSKF 181
| : : : | : : : | : : : | : : : | : : : |
201 ADMNE...PRCCSTCKYNVKNKEDHFLNNINVPNNMMSRTRIFYCTHF 247
| : : : | : : : | : : : | : : : | : : : |
2182 SEFNEYQLGKYCTES..QRKKTMFRLYSVTNKQKWQTKKK..... 220
| : : : | : : : | : : : | : : : | : : : |
248 NRNNQFFKKHBFVSNKNNISAMDRAQTIPTNIFRFRNIRKKLKDVKIEKI 297
| : : : | : : : | : : : | : : : | : : : |
221 ..RKENLLTKLOAIKESDEKSKRETG....DIMNVEDAIALKAPVAMKKI 264
| : : : | : : : | : : : | : : : | : : : |
298 AYMLEKVKDPNPNFYLTKSCLPENWREKQKQIENLINKTREEKSKYEE 347
| : : : | : : : | : : : | : : : | : : : |
265 AKRONAMK.....KHMKAPKIPNSTLESKYLTFKD 294
| : : : | : : : | : : : | : : : | : : : |
348 LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKYVELNKHE 397
| : : : | : : : | : : : | : : : | : : : |
295 LIKFCHISEP.....KERVYKLGKYPKTEEBEYKAAFQGSASAPFN..PE 338
| : : : | : : : | : : : | : : : | : : : |
398 LIHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLLRWIFEDL 447
| : : : | : : : | : : : | : : : | : : : |
339 LAGKRMKIEISKTWENELSAKGNTAEVMDNLISSNQLPYMAMLRNLSN.. 386
| : : : | : : : | : : : | : : : | : : : |
448 VVSLIRCFPHYTEQOKSYSKYTYRKNIDWIMKMSIADLKKETLAEVQE 497
| : : : | : : : | : : : | : : : | : : : |
387 .....ILKAGVSD..... 394
| : : : | : : : | : : : | : : : | : : : |
498 KEVEEWKSLGFPAGKLRLIPKKTFRPIMTFNKKIVNSDRKTTKLTNT 547
| : : : | : : : | : : : | : : : | : : : |
395 .....TTHS 398
| : : : | : : : | : : : | : : : | : : : |
548 KLLNSHMLMLKTLKNRMFKDPPGFAVFNYYDDVMKKYBEFVCKWKVQGPKL 597
| : : : | : : : | : : : | : : : | : : : |
399 IVINK.....ICEPKAVENSKM 415
| : : : | : : : | : : : | : : : | : : : |
598 PFATMDIEKCYDSVNREKLSTFLTKTKLLSSDFWIMTAQILKRKNIVID 647
| : : : | : : : | : : : | : : : | : : : |
416 F..PLQFFSAIEAVN..EAVTKGFKAKK...RENMNLKGQIEAVKE..VVE 457
| : : : | : : : | : : : | : : : | : : : |
648 SKNFRKKEMKDYFRQKFQKIALEGGQYPTFLFSVLENEQNLDNAKKTIVE 697
| : : : | : : : | : : : | : : : | : : : |
458 KTDDEBKDM.....ELBQTEBEGFVKVNEGIGKQYINSIELAIK 496
| : : : | : : : | : : : | : : : | : : : |
698 AKQRNYFKKDNLLQPVINICQYNYINFNGKPYQTKGIPQGLCVSSILSS 747
| : : : | : : : | : : : | : : : | : : : |
497 IAVNKNLDEIKGHTAIPSDVSGSMSTSMGGAKKYGSVRTCLECALVGL 546
| : : : | : : : | : : : | : : : | : : : |
748 FYYATLESSLGFLRDESMNPNPNVNLMLRLTDDYLLITTQENNAVLFI 797
| : : : | : : : | : : : | : : : | : : : |
547 MVKQRCESKFYIFSSPSSQCNKCYLEVDL..... 576

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FIG. 13

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798 EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMSDVEEQNIVQDYCD 846
      : : : : : | | | : : : : : | : : : : :
577 .....PGDELRPSPWQKLLQEKGLGGG..TDFPYECIDEWTKNKTHTVD 617
      : : : : : | | | : : : : : | : : : : :
847 WIGISIDMKTLALMPNINLRIEGILCTLNLNMQTKKASMWLKKLKSFLM 896
      | | | | | : : : : : | : : : : : | : : : : :
618 NIVLSDMMIAEGYSDINVRGSSIVNSI.....KKYKDEVN 653
      : : : : : | | | : : : : : | : : : : :
897 NNITHYFRKTITTTDFANKTLNKLFISSGKYKMQCAKEYKD.HFKKNLAM 945
      | | | : : : : : | : : : : : | : : : : :
654 FNKIF...AVDLEGYG.....KCLNLGDEFNENNYIKIFGM 687
      : : : : : | | | : : : : : | : : : : :
946 SSMIDLEVSKIISVTRAPFFKYLVCNIKDTIFGEEHYDPDFLSTLKHPIE 995
      | : | : : : : : | : : : : : | : : : : :
688 SDSI.....LKFISAKQGGG.....NMVE 706
      : : : : : | | | : : : : : | : : : : :
996 IFSTKKYIFNRVC 1008
      : : | : : : : :
707 VI..KNFALQKIG 717

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FIG. 13
(CONTINUED)

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132 LSTQKQYFFQDEWNQVRAMIGNEL.FRHLYTKYLIFORTSE..GTLVQFC 178
      : : : : : | | | : : : : : | : : : : :
1 MSRRNQ.....KKQCAPIGNETNLDPVLQNLVEYKSIIEHYKTQQQOI 43
      : : : : : | | | : : : : : | : : : : :
179 GNNVPDHLKVNDKFDKKQKGAADMNPRCCSTCKYNVKNKEDHFLNNIN 228
      : : : | | : : : : : | : : : : : | : : : : :
44 KEEDLKLKFKNQDQDGNNGNDDEE.....NNSNKQCELLRRVN 84
      : : : : : | | | : : : : : | : : : : :
229 VPNWNNMKSRTIFYCTHFNRRNNQFPKKHEFVSNKNISAMDRAQTIFTN 278
      : : : : : | | | : : : : : | : : : : :
85 .....QIKQVQLIKK...VGSKVEKDLNLNEDENKKN 114
      : : : : : | | | : : : : : | : : : : :
279 IFRFNRIKKLKDVKIEKIAYLEKVDFNPNYYLTKSCPLPENWREKRQ 328
      : : : : : | | | : : : : : | : : : : :
115 GLSEQQVKEBQLRTITTEQVKYQNLVFNMDYQLDLNESGGHRRHRETDY 164
      : : : : : | | | : : : : : | : : : : :
329 KIENLINKTREESKYEELFSYTTDNKCVTOFINE.FFYNILPKDPLTG 377
      : : : : : | | | : : : : : | : : : : :
165 DTEKWFEISHDQK.....NYVSIYANQKTSYCWMLKDYFNK 200
      : : : : : | | | : : : : : | : : : : :
378 RNRKNFQKKVKYVELNKHLEIHKNLLEKINTREISWMQVETSAKHFYY 427
      : : : : : | | | : : : : : | : : : : :
201 NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID..... 242
      : : : : : | | | : : : : : | : : : : :
428 FDHENIYVLNKLRLWI..FEDLVVSLIRCFYVTEQOKSYSKTYYYRQNI 475
      : : : : : | | | : : : : : | : : : : :
243 VNFNNLCILALLRFLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290
      : : : : : | | | : : : : : | : : : : :
476 WDVIMKMSIADLKKETLAEVQKEVEEWKKSGLGPAFGKRLRIPKTTFRP 525
      : : : : : | | | : : : : : | : : : : :
291 FAVVFSHR.....HLQGIHLQVPCFAQYVLVNSSQISVKSQSLQ 330
      : : : : : | | | : : : : : | : : : : :
526 IMTFNKKIVNSDRKTKTLTNTKLLNSHMLKTLKNRMFKDPFGFAVFN 575
      : : : : : | | | : : : : : | : : : : :
331 VYSFSTDCLKLVD..TNKVQDYKFLQEFPRLTHVSQQAIPVSATNAVENL 738
      : : : : : | | | : : : : : | : : : : :

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FIG. 14

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576 DDVMKKYEEFVCKWKQVGQPKLF.FATMDIEKCYDS. VNREK 615
 379 NVLLKKVKH ANLNLSIPTQPNDFYFVNLQHLKLEFGLPNILTKQK 426
 516 LSTFL.KTTKLLSSDFWIMTAQILKRKNNI. VIDSKNFRKKEMK 657
 427 LENLLLSIQSKNLKFLRLNFTYVAQETSRKQILKQATTIKNLKNNKQ 476
 558 DYFRQKFQKIALEGGQYPTLFSVLEN. EQNDLNAKTLIVEAKQRNYFK 705
 477 EETPETKDETPSESTSGMKFFDHLSELTELEDFSVN.LQATQEIY. 520
 706 KDNLLQPVINIQQYNYINFNGKFKYQTKGIPQGLCVSSILSSFYYATLEE 755
 521 .DSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNI.YETLNN 564
 756 SSLGFLRDESMNPNPNVNLRLITDDYLLITTQENNAVLFIKELINVS 305
 565LKRCSVNISNPHGNI SYELTN.KDSTFYKPKLTINQE 500
 806 ENGFKFNMKKLQTSFPPLSPSKFAYGMDSVEEQNIQVDYCDWIGISIDMK 855
 601 LQHAKYTFK. . QNEFQFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ 648
 856 TLALMPNINLRIBGILCTNLNMQT. . KASMNWKK. . KLSFMLNNIITH 901
 649 NVNI.IASLLYPNNIQKNPNFKNLLFFKQFQQLKNLENVSINC 691
 902 YFRKTI. . . TTEDFANKTLNKLFISSGGYKYMCAKEYKDHFKKNLAMSSM 948
 692 ILDOHILNSISEFLEKNKKIKAPILKRYLLQYLLDYTKLFKTLQQLPEL 741
 949 IDLEVSXIIYSVT.RAFFKYLVCNIKDT. . IFGEHY 982
 742 NQYINQQLLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDP 791
 983 PDFFLS TLKHFIETPKKY IFNRVCMILKAKEAKLSDQCQSLIQ 1028
 792 DQNTVSDDSIKKILESISESKYHHYRLNPNPSSQSSSLIKSENEEIQELLK 840

FIG. 14
(CONTINUED)

4 DIDLDDIENLLPNITFNKYSSSCSDKKGCKTLKSGSKSPSLTI PK. 47
 617 NVKSAKIESSSLESLEDIDSLCKSIASCKNLQVNNI IASLLYPNNIQKNP 666
 48LQKQLEFYFSDANLYNDSFLRKLWLKSGEQRVE. . . IETLLM 86
 667 FNKPNLLFFKQFQQLKNLENVSINCI LDQHILNSISEFLEKNKKIKAPIL 716

FIG. 15

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1 MEMDIDLDDIENL.....LPNTFNKYSSSSCKKGCKTLKSGSKSPS... 42
  | : | . . . | | . . . . . | : | . . . . . | | : |
491 IELAIIKIVNKNLDEIKGHTAIFSDVSGSMSTSMGGAKKYGSVRTCLEC 540

43 .LTIPKLQKQ.....LEFYFSDANLYNDSFLRKLVLKSGEORVEIETLL 85
  | : | : | | | | : | : | : | : | : | : | : | : | : |
541 ALVLGLMVKQRCCKSSFYIFSSPSSQCNKCYL.EVDLPGLDELRFSPMKLL 589

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FIG. 16

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telomerase p43 LQKQLLEFYFSDANLYNDSFLRKLVLKSGEORVEIETLLM
human La ICHQHEVYHGDHNLPRKFLKEQI.KLDEGWWPLEIMIK
Xenopus LaA ICEQHEVYHGDHNLPRKFLKQOI.LLDDGWWPLEMTIK
Drosophila La ILRQHEVYHGDANLNRKFLREQIGKNEDGWWPLSLVLT
S. c. Lhpip CLKQHEVYHSEFNFPYLRFLRTAEK.NDGWPISTIAT

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FIG. 18

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1 aactcattta attactaatt taactcaacaa gattgataaa aagcagtaaa taaaaccctaa
61 tagatttaatt tagaagaagta tcaattgaaa aatggaaaatt gaaacacaact aagcacacaata
121 gccaaaaagcc gaaaaaattgt ggtgggaact tgaaatagag atgcaagaata accaaaatgag
181 tatataagtt aggggttaaga ttgacgaccc taagcaaat atcgtgaacg tcaactgcagc
241 atgtctgttg taggaaggtta gttactacta agataaagat gaaagaagat atatcatcac
301 taaagcaact ctgaggtggt ctgaggtctga tccgtgattc atctgctagt tggcagctcta
361 catcggaat gaacttatac tcagaactac cactaactac attgtagat tttgtgtgt
421 ccacaagaat actcaacct tcactgaaaa gtacttcaac aaagcagtc ttttgcttaa
481 tgactctact gaagttctgt aatttgtaata ggtttctctat attttgtag caactgaatt
541 caaaaatttg tatcttgata ggatacttcc ataagataatt cgtaaggaac tcaatttcgc
601 taagtgttta caaagatggt tcagaagcaa gtttctgaa tccaacgaa actaatgtg
661 taagtattgc actgaatcct aacgtaaaga aacaatgttc cgttacctct cagttaccaa
721 caagtaaaag tgggattaaa ctaagaagaa gagaaaaagat aatctcttaa ccaaacctta
781 ggcaataaag gaactctgaag ataagtcгаа ggagaaact ggagacataa tgaaacttga
841 agatgcaact aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
901 catgaagaaa caactgaagg caactaaaat tcttaactct accttgaaa caaagtaact
961 gaactcaag gatctaatia agttctgcaa tattcttgag cctaagaaga gactctataa
1021 gatccttggt aaaaaatacc ctaagaccga agaggaatac aaagcagct tttgtgtatc
1081 tgcactctga ccttcaactc ctgaattggt tggaaaagct atgaagattg aaactcttaa
1141 aacatgggaa aatgaactca gtgcaaaagg caacactgt gaggtttggg ataatttaat
1201 tcatgaagat taactcccat atatggcat gttacgtaac ttgtctaaac tcttaaaagc
1261 cgggtgttca gatactacac actctattgt gatcaacaag atttgtgag ccaaggcgt
1321 tgagaactcc aagatgttcc ctctcaact ctattagtc attgaagctg ttaatgaagc
1381 agtcaactaa ggaactcaagg ccaagaagag agaaaatgat aactctaaag gtcaaatcga
1441 agcagtaagg gaagtgtgtg aaaaaaccga gtttctgaa aaagatctga agtgcaggtg
1501 aaccgaagaa ggagaatttg ttaagtcгаа cgaaggaatt ggcaagcaat accataactc
1561 cattgcaact gcaactcaaga tagcagttta caagaattta gatgaataca aaggacacac
1621 tgcactcttc ttgatgtgtt ctggttctat gagtacctca atgtcaagtg gagccaagaa
1681 gtatgtgttc gttgttaact gtctcagtg ttctattgta tggtaaaata tggtaaaata
1741 acgttgtgaa aagctcctat tctacatctt cagttcaact agtttctaat gcaataagtg
1801 ttaactagaa gttgatctcc ctggagacga actcgtctct tctatgttga acttttgc
1861 agagaaagaa aaacttggtg gtggtactga ttccccat gagtgcatg atgaatggac
1921 aaagaataaa actcagtag acaatctcgt tatcttctgt catgatgat tgcagaag
1981 atattcgat atcaatgtta gaggaagtc catgttaac agtataaa agtataaaga
2041 tgaagttaat cctaactata aaactcttgc agtgcatt caaggttaac gaaggtgct
2101 taactctagt gatgagttca atgaaaacaa ctacatcaag atattcgta tgcagcttc
2161 aatctctaa gttatttgc ccaagcaag agggcaaat atggtcga ttaacaaaaa
2221 ctttgccttc caaaaaatag gacaaaaagt agttcttga gattctcta tatcctattt
2281 ctaacccac tttttgttt tattgcatg ccattatgaa atttaaat tttctattt
2341 atttaagtta cttaatagt ttatgtatgc gctatctaa atgattctgc
2401 aaagaacaaa aaagattaaa a

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FIG. 19

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FIG. 17

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MEIENNOAQOPKAEBKLWWELEEMQENQNDIQVRVKIDDPKQYL
VNUYTAACLLQGGSSYQODKDERRYITKALLVVAESDPEFCOLA
VYIRNELYIRTYNYIVAFQVVEKNTQPFIEKYFNKAVILLPNL
LEVCEFAQVLYI PDATPEKNLYLDRI LSQDIRKBLTFRKCLQRC
VRSPFSEFNEVQLKYCTESQORKKTMFRYLSVTNKQKQWQDTKKK
RKENLLTKLQAIKESBEDKSRETDGIMNVEDA IKALKPAVMKKI
AKRONAMKHKMKAPKIPNSTLESKYLTFKDLIKPCHISBPKEV
KYILGKKYKPTBEEYKAAFGDSASAPPNELAGKMKMIIESKTW
ENELSAKGNTEVWVNDL ISSNQLPYMAMLRNL SNILKAGVSDTT
HSIVINKICEPAVENSKMFPLOFSAIEAVNEAVTKGFKAKKR
ENMNLKGQIEAVKEVEKTDDEEKMDMLBQTEEGEPVKVNEGIG
KQYINSIELAIAIVANKNLDEIKGHTAIPSDVSGSMSTSMGGGA
KKYGSVRTCLBCALVLGLVMVKQRCESKSSFYIFSSPSSQCNKCYL
EVDLPQDELRPSMQKILQEKKGKIGGGTDPPEYCEIDEWTKNKTTHV
DNIVILSDMMIABGYSIDINVRGSSIVNSIKKKYKDEVNPNIKI PA
VDLEGYGKCLNLGDEFNENNYIKIFGMSDSILKPI SAKQGGANM
VEVIKNFALQKIGQK

FIG. 20

MSRRNOKKPOAPIGNETNLDVFLQNLLEVYKQIEHYKTQQOQIK
EEDLKLKFKNQDQDGNSGNDDDDENNNSKQOELLERVNQIKQ
QVOLIKKVGSKVEKDLNLNEDENKKNGLSEQOVKEBOLRTITTE
OVKYONLVFNMDYQLDNLNSEGGRHRHRETDYDTEKWFISHDO
KNYVS IYANQKTSYCWNLKDYFNKNYDHLNVSNRLETEAEFY
APDDFSQTIKLTNNYSQTVNIDVNFNNLCLIALLRFLLSERF
NILNIRSSYTRNQVFEKIGELLETI PAUVFSHRHLQGIHLQVP
CEAPOYLVNSSSQISVKDSQLOVYSFSTDLKLVDTNKVQDYKPF
LOEFPRLTHVSOQAI PVSATNAVENLNLVKKVKHANLNLVSI P
TQPNDFPYFVNLQHLKLEFGLPENILTKQKLENLLLSIKQSKNL
KFLRANFYTYVAQTSRKQILKQATIKLKNKNQOETPETKD
ETPSESTSGMKFPDHLSELTELEDFSVNLQATQBIYDLSHLKLI
RSTNLKPKFLGYKYEKESKMDTFIDLKNIYETLNNLKRCSVNI
SNPHGNISYELTNKDSYFYKFKLTNLQELQHAKYTFKQNEPQFN
NVKSAKIESSSLESLEDIDSLCKSIASCNNLQNVNIIASLLYPN
NIQKNPFPKNPLFFKQPEQLKNLENVS INCILDQHILNSISEF
LEKNKIKAFILKRYLLQYLYLDYTKLFTLQLOPELQVYINQ
OLEELTVSEVHKQVWENHKKQAFYEPLCEFTIKESSQTLQIDIFD
QNTVSDDS IKKILESSEKYHHYLRNLNPSQSSSLKSENEBEQ
ELLKACDEKGVLVKAYYKFLCLPTGTYYDYNSDRW

FIG. 22

MKILFEPIDQKLDIDLQTNSTYKENLKGHFNGLDEILTTCFAL
PNSRKIALPCLPGDSLHKAVIDHCHIIYLLTGELYNVNLTFGYKI
ARNEDVNNLSFCHSANVNVTLKGAAMKMFHSLVGTYAFVDLLI
NYTVIQFNGQFFQTIQVGNRCNEPHLPKQVQVRSSSSATAAQIK
QLTEPVTNKQFLHKLININSSSFFPYSKI LPSSSSIKKLTDLREA
I PFTNLVKIPORLKVRIINLTQKLKRHKRLNVYSI LNSICPPL
EGTVLDSLHLSRQSPKERVLPKPIIVILQKLLPQEMFGSKNKGK
IIKMLNLLSLPLNGYLPFSDSLKLRKLKDFRMLFISDIWFTKH
NFENLNQALQFISWLFRLQILPKIQTFYCTEISSTVTIVVFR
HDTWNLKLTPTFIVEYFKTYLVENWVRHNSYVLSNPNHKSQWRI
IPKKSNNENPRIIAIPCRGADDEEPTTYKENHKNIAQPTOKILEY
LRNKRPTSPFTKIYSPTQIADRIKEFKORLLKFFNVLPLEYFMYK
FDVKSCYDSI PRMECMRILKDALKNBNGFVFRSQQYFPNTNTGV
KLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINNVEMEIPKTA
LWVEDKCYIRDEGLFQSSLSAPIVDLVYDDLLEYFSEFKASPS
QDTLILKLADDFLIISTDQOQVINIKKLAMGGQFKYNAKANRDK
TLAVSSQSDDDTVIQFCAMHIFVKELEVWKSHTMNNPHIRSKS
SGIIFRSLIALFNTRISYKTDITNLMNSTNTVLMQIDHVVKNISE
CYKSAFKDLSINVTVNQMPHSFLQRIIBMTVSQCCPTKCDPLIE
YEVFTIILNGLFELSSENTSKFKDNIILLRKEIHLQIAYIYYI
HIYN

FIG. 23

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1 tcaatactact taattaataa ataaaaaaa gcaaaactaca aagaaaaatgt caaggogttaa
 61 ctaaaaaaaag ccataggctc ctataggcaa tgaacacaaat cttgatttttg tattacaaaaa
 121 tctagaagtt tacaaaagcc agcttgagca ttataagacc tagtagtaac agatcaaaaga
 181 ggaagatctc aagcttttaa agttcaaaaa ttaagatag gatgaaac ctggcaacga
 241 gatgatgat gaagaaaaca actcaataaa ataataaaga ttattaaaga gagtcaatta
 301 gattaaagtag caagttttaa tgataaaaaa agttggtctc aaggttagaga aaagtttgaa
 361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgtaa tgaocaaatga aagaagagta
 421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta
 481 ccagttagat ttaaatgaga gtgggtggcca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tgggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttagcccaa
 601 ctaaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaaa attatgatca
 661 tcttaaatgta agcattaaaca gactagaaac tgaagcogaa ttctatgctt ttgatgtatt
 721 ttccacaaca atcaaaacta ctaataatct ttactagact gttaacatag acgttaattt
 781 tgataaataat ctctgtatcc tgcgattgtc tagattttta ttatcaatag aaagattcaa
 841 tattttgaat ataagatctt ctatatacag aaattaatat aattttgaga aaatttggtga
 901 gctacttgaa actatcttcg cagttgtctt ttctcatcgc cacttacaag gcattcattt
 961 acaagttcct tgcgaagcgt tctaatattt agttaactcc tcatcataaa tttagcgttaa
 1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaacaa
 1081 agtccaagat tatttttaagt tcttataaga attccctcgt ttgactcatg taagctagta
 1141 ggcataccca gttagtgcata ctaacgcgtg agagaacccc aatgttttac ttaaaaaggt
 1201 caagcgtcgt aatcttaatt tagtttctat cctactctaa ttcaaatttg attttcactt
 1261 tbttaactta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaa
 1321 aaagcttgaa aatctacttt tgagtataaa ataatacaaa aatcttaaat tttaaagatt
 1381 aaacttttac acctacgttg cttaagaaac ctccagaaaa cagattatcaa aacaagctac
 1441 aacactcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaagatga
 1501 aactccaagc gaaagcacia gtggtatgaa attttttgat catctttctg aatttaocga
 1561 gcttgaagat ttacagcgta acttgtaagc taccacaaga atttatgata gcttgacaaa
 1621 acttttgatt agatcaaaaa atttaaaaga gtccaataa agttaacaat atgaaatgga
 1681 aaagagttaa atggatacat tcatagatct taagaatat ttatgaacac taacaacat
 1741 taaaagatgc tctgttaata tatcaaatcc tcatggaaac atttcttatg aactgacaaa
 1801 taagattctt actttttata aatttaagct gacottaaac taagaattat aacacogctaa
 1861 gtatctcttt aagtagaacg aatttttaatt taacaacgct aaaaagtgcaa aatttgaaat
 1921 ttctctacta gaaagcttag aagatatgga tagcttttgg aaattcttga actttgttaa
 1981 aattttacaa aatgttaata ttatcgccag ttgtcttat ccccaacata tttagaaaaa
 2041 tcttttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaaatttgg
 2101 aatgtatct atcaactgta ttcttgatca gcatataact aattctattt cagaattctt
 2161 agaaaaagaa aaaaaataa aagcattcat ttgaaaaga tattatttat tacaatat
 2221 tcttgattat actaaattat ttaaaacact tcaatagta cctgaattaa attaagttta
 2281 catttaattg caattagaag aattgactgt gagtgaagta cataagctta tatgggaaa
 2341 ccaacagcaa aaagctttct atgaacccat atggaggttt atcaaaagat catctctaac
 2401 cctttagcta atagattttg acccaaaacac tgttaagcgt gactctata aaaaagatt
 2461 agaatctata tctgagctca agtatcatca ttatttgaga ttgaacocct gttaatctag
 2521 cagtttaatt aaactctgaa acgaagaaat ttaagaact ctcaagcct gcgacgaaaa
 2581 aggtttttta gtaaaagcat actataaatt cctcttatgt ttccaactg gtaactatta
 2641 cgattacaat tcaagatagat ggtgatata taatatattg tttaaatcaa tattaaatat
 2701 tgaatttttc ttgttttatt atttgataaa tacatacaat agtcaatttt aggtttttga
 2761 ataatattta gttattttaa tcatattttt aagtaataaa ttatttttca atctattttt
 2821 aaaaaatcg

FIG. 21

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LCVSYILSSFPYYANLEENALQFLRKESMDPEKPETNLLMLRLT
LCVSSILSSFPYYATLEESSLGLPLRDESMNPENPNVNNLLMLRLT

FIG. 24

ATTTATACTCATGAAAAATCTTATTGCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAGAAAAATTTAAATGTGGTCACTTCAATGGCCCTCGATGAAAT
TCTAACTACGTGTTTCGCACTACCAAATTCAGAAAAATAGCATTACCATGCCCTTCCTGG
TGACTTAAGCCACAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGGCAAT
ATACAACAACGTAATAACATTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
TCTTTTTGCGCATCTGCAAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAAT
GTTCCACAGTTTGGTCGCTACATACGCATTTCGTTGATTTTATTGATCAATTATACAGTAAT
TCAATTTAAATGGGCACTTTTCACTCAAAATCGTGGGTAAACAGATGTAAACGAACCTCATCT
GCCGCCCAATGGGTCCAAACGATCATCCTCATCATCGCAACTGCTGCGCAAAATCAACA
ACTTACAGAAACCAAGTGACAAATAAACCAATCTTACACAAGCTCAATATAAAATCTCTCTC
TTTTTTTCCCTATAGCAAGATCCTCTTTCATCATCATCTATCAAAAAGCTAACTGACTT
GAGAGAGCTATTTTTCCCAAAATTTGGTTAAAAATCTCTCAGAGACTAAAGGTACGAAT
TAATTTGACGCTGCAAAAAGCTATTAAAGAGACATAAGCGTTTGAATTCAGTTTCTATTTT
GAATAGTATTTGCCACCATTTGGAAGGGACCGTATTGGACTTGTGCGCATTTGAGTAGGCA
ATCACCAAGGAACGAGTCTTGAAATTTATCATTTGTTATTTTACAGAAGTTATTACCCCA
AGAAATGTTTGGCTCAAGAAAAATTAAGGAAAAATTTATCAAGAACTCAAACTCTTTATT
AAGTTTACCTTAAATGGCTATTTACCATTTGATAGTTTGTGAAAAAGTTAAGATTAA
GGATTTTCGTTGGTTGTTCTATTTCTGATATTGGTTTACCAAGCACAATTTTGAAAACTT
GAATCAATTGGCGATTGTTTCATTTCTGGCTATTTAGACAACATAATTCACAAAATTTAT
ACAGACTTTTTTTTACTGCAACCGAAATATCTTCTACAGTGACAATTTGTTTACTTTAGACA
TGATACTTGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTAATCTAGT
CGAAAAACACGATATGAGAAACCAATAAGTTACACGTTTGTCCAATTTCAATCATAGCA
AATGAGGATTATACCAAAAAAAGTAATAGTGGTTGAGGATTTTGGCCATCCCATGCGAG
AGGGGCAGACGAAGAAGAAATTCACAAATTTATAAGGAGAAATCACAAAAATGCTATCCAGCC
CACTCAAAAAATTTTAGAATACCTAAGAAAAACAAAGGCGCAGTATGTTTACTAAAAATATA
TTCTCCAAACGCAAAATAGCTGACCGTATCAAGAAATTTAAGCAGAGACTTTTAAAGAAAT
TAATAATGTCCTTACCAGAGCTTTATTTTATGAAATTTGATGTCAAATCTTGCTATGATTC
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAATGAAAAATGGGTT
TTTCTGTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAATTTATTAAATGT
TGTAAAGCTTACGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTTTACAAATCAGGATGTTATAAGCTTTGAGAGATGGAATAATTTAAACACGCTT
GTGGGTTGAAGATAAGTGCTACATAGAGAAAGATGTCCTTTTACAGGCTCAAGTTTATC
TGCTCCGATCGTTGATTTTGTGTATGAGCATCTTCTGAGATTTTATAGCAGTTTAACT
CAGTCTTACAGGACACATAATTTTAAACCTGCTACGCAATTTCTTATAAATCAAC
AGACCAACAGCAAGTATCAATATCAAAAAGCTTGCATGGGCGGATTTCAAAAATATAA
TGCGAAGCCAAATAGAGACAAAATTTTACCGGTAACTCCAATCAGATGATGATACGCT
TATTTCAATTTTGTGCAATGACATATTTTGTGTAAGGAATTTGGAACATTTCAAG
CAATAGAAATAATTTCCATATCGTTTCAAAATAGTAAGGGATTTTTCAGATTTTAA
AGCGCTGTTTAAACACTAGAATCTCTTATAAAACAAATTTGACACAAATTTAAATTTCAACAA
CACGCTTCTTACGCAAAATGATCATGTTGTAAGAACATTTGCAAGATGTTTAAATCTGC
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTTCAATCGTTTCTTAAACG
CATCATTTGAATGACAGTCAGCGGTTGTTCAATTTAGAAATGATGCTTTTAACTGAGTA
TGAGGTACGATTCACATATTTGAATGGATTTTGGAAAGCCCTATCTTCAACACATCAAA
ATTTAAGATAATATCATTTCTTTGAGAAAGGAATTTCAACACTTGCAAGC

FIG. 26

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AKFLHWMLSVYVVVELLRSSFYVTETTTFQKNRFFFYRKSVMKLSQSIGIROHLKR
VQLRVDSEAEVRQHRERAPALLTSRLRFIPKPDGLRPIVNMDDYVVGARTFREK
RAERLTSRVKALFSVLNVERA

FIG. 27

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTAAGTCTGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCAAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAGCATTGGGAATCAGACAGCACTTGAAG
AGGGTGCAGCTGCGGACGTGTGCGAGCAGAGGTGAGGACATCGGGAAGC
CAGGCCGCGCTGTGACGTCCAGACTCCGCTTCTATCCCAAGGCTGACGGGC
TGCGCCGATTTGTGAACATGGAAGTCTGCTGCGAGCAGAACGTTCCGAGA
GAAAGAGGGCGGAGCGTCTCACTCGAGGTTGAAGGCACTGTTCAAGCTGCT
CAACTACGAGCGGGCGCG

FIG. 28

MTEHHTPKSRILRPLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSQVTSFSIFLHSTVVG
DSKPDGCVQSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFMSNHEDFRAMHVNGVQNDLVST
PNYLISILESKNQWLLLEIGSDAMHYLLSKGSIPEALPNNDYLOIGSIFLKNVVEETVSKRRR
TIETSIQNKSAKREKSVNSISIRSFISIFRSSYKFKQDLYPNLHSCDRNTVHMLQWIPRQFG
LINAPQVKQLHKVPLVVSQSTVVPKRLLKVYPLIEQTAKRLHRSLSKVYNYHCYPIDTHDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFFIILKDLFTFLKLSRYESFSLHYLMSNIIKISEIWL
VLGKRSNAKMLSDFEKRQIFAEFIYWLNSFIIPILOSFYITESSDLNRNTVYFRKDIWKLRCR
PFITSMKMEAFEKINENNVRMDTQKTTLPAPVIRLLPKKNTFRLITNLRKRFLIKMGSKNKLVSNTN
QTLRPVASILKHLINEESSGIPFNLEVMKLLTFKKDLLKHRMFGKKYFVRIDIKSCYDRIKQDLM
FRIVKKLKDPFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVQQLSMKTSDTLFDVFDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVDDFLFITVNNKDAKKFLNLSRGFEKHNFTSLEKTVINFENSNGIINNTFFNESKKRMPPFG
FSVNMRLDTLLACPKIDEALFNSTSVELTKHMGKSPFYKILRSSLASFAQVFIDITHNSKFNSCCN
IYRLGYSMCMRAQAYLKRMDIFIPQRMFITDILLNVIGRKWKLAELGYTSRRFLSSAEVKWLF
LGMRDGLKPSFKYHPCFQLIYQFSLTDLIKPLRPVLRQVLFLHRIAD

FIG. 29

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FIG. 30

EST2 pep	FFXTEISST VTIWFRHDT WN---KLIT P-----PIVE YFK-TYLVEN	40
Euplates pep	FFVTEOOSK YSKTYVVRN IMDI-MKMS IAD---LAK ETLA-EVOE	43
Trans of tetrahymen	-----KHKE GSQIFYVRKP IMELVSKLTI VKVRIQFSEK NKOMNNFYQ	44
Consensus	FFY.TE..K..S..YYVRK.IW...-KL...-----F..K.....V..	50
EST2 pep	NVCRNHSY- -----TLSNFNHSN RHIPKRNNE FRUAIIPCRG	79
Euplates pep	KEVEEMKSL ----- --GFAGGK RLTPKNT-- FRPMTFNKK	78
Trans of tetrahymen	KIQLEENLR KVEEKLPED SFQYPOGML RHIPKRS-- FRPMTFLRK	92
Consensus	K..E.....-...F..GGL-RHLPKR...--FRPMTFLRK	100
EST2 pep	ADREPTLYK ENHNAIOPT OKILEYFANK RPSTFTLYS PTQIADRIE	129
Euplates pep	IVNSDEKTK LTTNKLANS HLMATLAKN- -----DMEK -DPGPAVEN	130
Trans of tetrahymen	DIQKNIK---LNLNQILMDS QLVFNKAD- -----NL-G -QKIGSVDP	130
ConsensusK.K.LN.N.L..S.QL.L.LAKN- -----...IG..VF..	150
EST2 pep	FKORLLKEN NVL-----PFLFMKFD VKSCYD	157
Euplates pep	YD-DVMKVE EFVCKWQVH CMLFPATMD IEKCYD	155
Trans of tetrahymen	NK-QISEKFA QFIEKWKNG RPLFYVITL- -----	158
Consensus	.K...KFF..F..KWK..G..PFLFY.T.D...CYD	166

FIG. 31

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S-1: FFY VTE TTF QKN RLF FYR KSV WSK
 S-2: RQH LKR VQL RDV SEA EVR QHR EA
 S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
 A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
 A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

FIG. 32

Poly 4

	t	a	a	g	c	c	c	g	
5'-	cag	acc	aaa	gga	att	cca	taa	gg	-3'
	Q	T	K	G	I	P	Q	G	

4 (B')

5 (c')

	D	D	Y	L	L	I	T	
3'-	ctg	ctg	atg	gag	gag	tag	tg	-5'
	a	a	a	a	a	a	a	
			t	t	t	t	t	
				c	c			

Poly 1

FIG. 34

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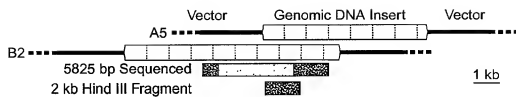


FIG. 33A

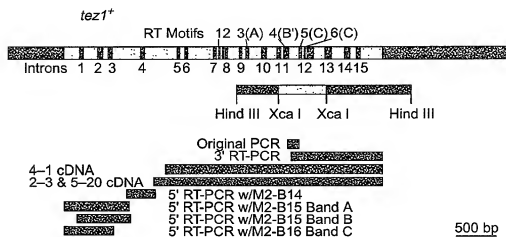


FIG. 33B

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20140526250010054205-041102

201140-56245001

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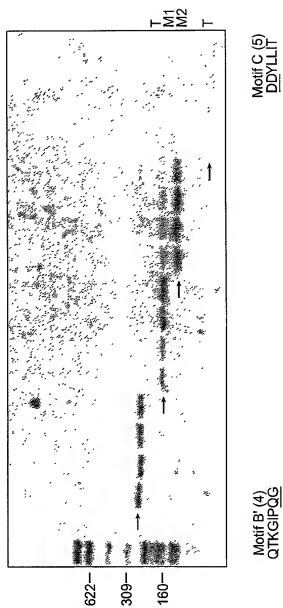


FIG. 35

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GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
 CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC CCT AGT CAC AAC AAT GCT
 E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc
 CAT CAG ctg ctg atg gag gag tag tgg

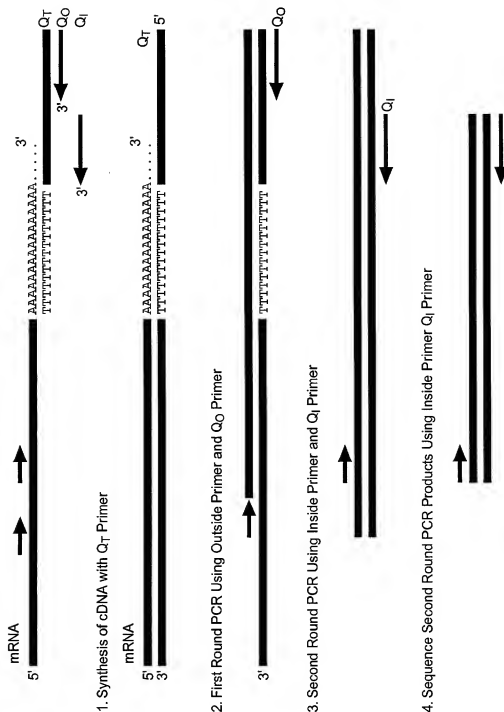
V V D D Y L L I T

<---- ctg ctg atg gag gag tag tgg
 a a a a a a a
 t t t t t
 c c c
Poly I

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence
 D D F L F I T

FIG. 36
 (CONTINUED)

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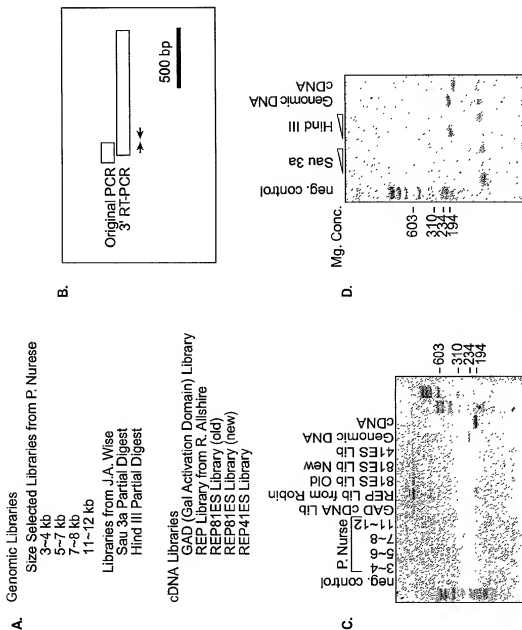


FIG. 38

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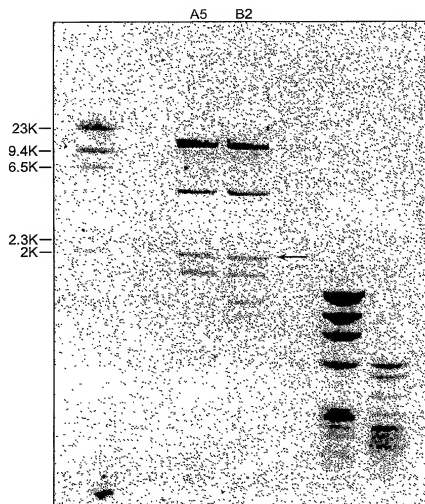


FIG. 39

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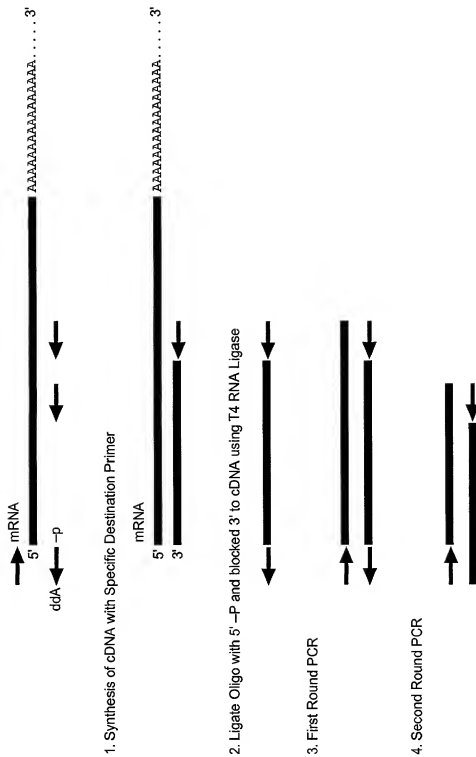


FIG. 40

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Motif O

S.p. Tes1p (429) . WLYNSFIPILOSFYITESSDLRNETVYFRKDIW ... (35) ...
 S.c. Est2p (366) . WLFRLPIKPIQTFFYCTEISSTVT-IVYFRHDTW ... (35) ...
 E.a. p123 (441) . WIFEDLVSLRCFFVYTEQKSYSTYYFRKIW ... (35) ...

Motif 1 Motif 2 K
 p hh h k hr h R

S.p. Tes1p AVIRLLPKK--NTFRLLTN-LRKRF ... (61) ...
 S.c. Est2p SKMRIIPKSGNNEFRIIAIPCGAD ... (62) ...
 E.a. p123 GKRLRIPKK--TFRPIMTENKKIV ... (61) ...

* *** ** *

Motif 3(A) AF
 h hDh GY h

S.p. Tes1p KKYFVRIDIKSCYDRIKDLMFRIVK ... (89) ...
 S.c. Est2p ELYFMKFDVKSCYDSIPRMECKRILK ... (75) ...
 E.a. p123 KLEFATMDIEKCYDSVNRKLSLTELK ... (107) ...

* * *** *

Motif 4(B')

hPQG pp hh h

S.p. Tes1p YLQKVGIPQSSILSGFICFYMEDLIDEVLSF ... (6) ...
 S.c. Est2p YTREGLEFQSSLSAPVDLVVDLLREVSF ... (8) ...
 E.a. p123 YKQIKGIPGLCVSSILSGFYATLESSLGF ... (14) ...

* *** *

Y Motif 5(C)
 h F DdhHh Gh h ck h

S.p. Tes1p VLLRVDDFLFITVKKDKAKFLNLSRGFEKHNFSTSLKTIINFENS . (205)
 S.c. Est2p LILKLADDFLIISTQOQVINIKLAWGGFKYNAKARDKILAVSSQS . (173)
 E.a. p123 LLMRLLTDYLLITTOENNAVLFTKILINVSRENGKFNMKLQTSFFLS . (209)

*** *

FIG. 41

FIG. 42

(CONTINUED)

A.	Sp_Tip1p	426	E	F	I	Y	W	L	Y	N	S	E	I	I	P	I	L	Q	S	F	F	Y	I	T	E	S	S	D	L	R	N	R	I	V	Y	458	
	Sc_Est2p	363	C	F	I	S	W	L	F	R	Q	L	I	P	K	L	I	Q	T	F	F	Y	C	T	E	I	S	S	T	V	T	-	I	V	Y	394	
	Ea_p123	438	K	L	L	R	W	I	E	D	I	V	S	L	I	R	C	F	F	Y	V	I	E	Q	Q	K	S	Y	S	K	I	Y	Y	Y	470		
	Sp_Tip1p	459	F	R	K	D	I	W	K	L	L	C	R	P	F	I	T	S	M	K	W	E	A	F	E	K	I	N	E	N	N	V	R	M	D	491	
	Sc_Est2p	395	F	R	H	D	I	W	N	K	L	I	T	P	E	I	V	E	Y	E	K	I	Y	L	V	E	N	N	V	C	R	N	H	N	S	427	
	Ea_p123	471	Y	R	K	N	I	W	D	V	I	M	K	M	S	I	A	D	L	K	K	E	T	L	A	E	V	Q	E	K	E	V	E	E	W	503	
	Sp_Tip1p	492	T	Q	K	T	T	L	P	A	V	I	R	L	L	P	K	K	-	-	N	T	F	R	L	I	T	N	L	R	K	R	F	L	522		
	Sc_Est2p	428	Y	T	L	S	N	F	N	H	S	K	M	R	I	I	P	K	S	N	N	E	F	R	I	I	A	I	P	C	R	G	A	D	480		
	Ea_p123	504	K	K	S	L	G	E	A	P	G	K	L	R	L	I	P	K	K	-	-	T	T	F	R	P	I	M	T	F	N	K	I	V	534		
	Sp_Tip1p	523	I	K	M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	V	A	S	I	L	K	H	L	I	N	E	-	-	552		
	Sc_Est2p	461	E	E	E	-	-	F	I	I	Y	K	E	N	H	K	N	A	I	Q	P	T	Q	K	L	L	E	Y	L	R	N	K	R	P	T	491	
	Ea_p123	535	N	S	D	-	-	R	K	T	T	K	L	T	N	T	K	L	L	N	S	H	L	M	L	K	T	L	K	N	R	-	M	F	564		
	Sp_Tip1p	553	E	S	S	G	I	P	F	N	L	E	V	Y	M	K	L	T	F	K	K	D	L	L	K	H	R	M	F	G	R	-	K	K	584		
	Sc_Est2p	492	S	F	T	K	I	J	Y	S	P	T	Q	I	A	D	R	I	K	E	F	K	Q	R	L	L	K	K	F	N	N	V	L	P	E	L	524
	Ea_p123	565	K	D	P	F	G	F	A	V	F	N	Y	D	I	V	M	K	K	Y	E	E	F	V	C	K	W	K	Q	V	G	Q	P	K	L	587	
	Sp_Tip1p	595	Y	F	V	R	I	D	I	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	K	L	K	D	P	E	-	F	616	
	Sc_Est2p	525	Y	F	M	K	F	D	V	K	S	C	Y	D	S	I	P	R	M	E	C	M	R	L	L	K	D	A	L	K	N	E	N	G	F	557	
	Ea_p123	598	F	E	A	T	M	D	I	E	K	C	Y	D	S	V	N	R	E	K	L	S	T	F	L	K	T	T	K	L	S	S	D	E	630		
	Sp_Tip1p	617	V	L	R	K	Y	A	T	I	H	A	T	S	D	R	A	T	K	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	634		
	Sc_Est2p	558	F	V	R	S	Q	Y	F	F	N	T	N	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	570			
	Ea_p123	631	W	I	M	T	A	Q	I	L	K	R	K	N	I	V	D	S	K	N	F	R	K	K	E	M	K	D	Y	F	R	Q	K	663			

FIG. 42

(CONTINUED)

A.	Sp_Tip1p	635	[FVSEAFSYFDMVPFEKVVQLLS--MKTSDILFLV]	665
	Sc_Est2p	571	-----VLKLFNVNASR--VPKPYELIY	591
	Ea_p123	664	[FQKI[ALEGGQYPTLESVLENEQNDLNAKKTLIV]	696
	Sp_Tip1p	666	[DFVDYWTKSSSEIFKMLKEHLSGHI VKIGNSQY]	698
	Sc_Est2p	592	DNVIRIVHLSNQDVINVVEMEIFKIALWVEDKCY	624
	Ea_p123	697	EAKQRNYFKKDNLLQPVINICQYNYINFGKIFY	729
	Sp_Tip1p	699	LQKVGILPQGSILSSFLCHFYMEDLI DEYLSFTK	731
	Sc_Est2p	625	LRDGLLEFGSSLSIAPIVDLVYDDLLEFYSEFKA	657
	Ea_p123	730	KQTKGILPQGLCVSSILSSFYATLEESLSGELR	762
	Sp_Tip1p	732	KKG-----SVLLRVVDDFLFITVNKKDAKK	756
	Sc_Est2p	658	SP[SQD-----TLILKLADDELIIISTDQQQVIN	684
	Ea_p123	763	DES MNPENPNVNL LMR LTDDYLLITIQENNAVL	795
	Sp_Tip1p	757	[ELNLSLRGFEKHNFESTSLEKTVIN[EN]SNG---	786
	Sc_Est2p	685	JKKLLAMGGFQKYNNAKANRDKILAVSSQSD---	713
	Ea_p123	796	[FIEKLINVSRENGEFKNMKKLQTSFPLSPSKFA	828
	Sp_Tip1p	787	---IINNNTFF[N]ESKKRMPFFGFSVNMRS[LD]TLL	816
	Sc_Est2p	714	---DDTVIQFCA--IMHIFVKELEVWKHSSTM	739
	Ea_p123	829	KYGMDSVEEQNI VQDYCDWI[GISIDMKTLALMP	861
	Sp_Tip1p	817	ACPKI[DEALFNSTSVELTKHMGKSF FYKILRS	849
	Sc_Est2p	740	NNFH[IRSKSKGIFRSLIALFNTRISYKTTIDIN	772
	Ea_p123	862	ININLR[IEGILCTNLNMQTKKASMWLKKKLKSF	894

FIG. 42

(CONTINUED)

A.	Sp_Tip1p	850	L	A	S	F	A	Q	V	I	D	I	T	H	N	S	K	F	N	S	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R	882				
	Sc_Est2p	773	L	N	S	T	N	I	V	L	M	Q	I	D	H	V	V	K	N	I	S	E	C	-	-	-	-	-	-	-	-	-	-	-	-	793			
	Ea_p123	895	L	M	N	N	I	T	H	Y	F	R	K	I	T	T	E	D	F	A	N	K	T	L	N	K	L	F	I	S	G	G	Y	K	927				
	Sp_Tip1p	883	A	Q	A	Y	L	K	R	M	K	D	I	F	I	P	Q	R	M	F	I	D	L	N	V	I	G	R	K	I	W	K	K	915					
	Sc_Est2p	794	-	-	-	Y	K	S	A	F	K	D	L	S	L	N	-	V	T	Q	N	M	Q	F	H	S	F	L	Q	R	I	I	E	M	821				
	Ea_p123	928	Y	M	Q	C	A	K	E	Y	K	D	H	E	K	K	N	L	A	M	S	S	M	I	D	L	E	V	S	K	I	I	Y	S	V	960			
	Sp_Tip1p	916	L	A	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W	L	F	C	L	G	M	R	D	G	L	K	P	S	948			
	Sc_Est2p	822	T	V	S	G	C	P	I	T	K	C	D	P	L	I	E	Y	E	V	R	F	T	I	L	N	G	F	L	E	S	L	S	S	N	854			
	Ea_p123	961	T	R	A	F	F	K	Y	L	V	C	N	I	K	D	T	I	F	G	E	E	H	Y	P	D	F	F	L	S	T	L	K	H	F	993			
	Sp_Tip1p	948	F	K	Y	H	P	C	F	E	Q	L	I	Y	Q	F	Q	S	L	T	D	L	K	P	L	R	P	V	L	R	Q	V	L	F	981				
	Sc_Est2p	855	T	S	-	-	-	-	-	-	-	-	-	-	-	-	K	F	K	D	N	I	L	L	R	K	E	I	Q	H	L	Q	A	Y	I	877			
	Ea_p123	994	I	E	I	F	S	-	-	-	-	-	-	-	-	-	T	K	Y	I	E	N	R	V	C	M	I	L	K	A	K	E	A	K	L	K	S	D	Q
	Sp_Tip1p	982	L	H	R	R	T	A	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	988				
	Sc_Est2p	878	I	Y	I	H	I	V	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	884					
	Ea_p123	1024	Q	S	L	I	Q	Y	D	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1031				

FIG. 42
(CONTINUED)

B.	Sp. Tip1p	Sc. Est2p	Ea. p123
1	-----MTEHHTPKSRILRFL	ENQYVYLCT	74
1	MEVDVNDQADNHGIIHSA	LKTC EEIK	EA
1	MEVDVNDQADNHGIIHSA	LKTC EEIK	EA
25	NDYVQLVLRGSPA	SSVYSN	ICERL
8	IQDKLIDIDLQTN--	STYK--	ENLKC
34	IQKVICRNRQSQ--	SHYK--	DLEDIK
58	IFLHSTVVGFD	SKPDE	GVQV
36	EILTTFCALPNSR	KIALPC	LVPGDL
91	IVATPRDYNEED	KVIARKE	VPFSTGL
61	VVKQMFDES	FERR--	NLLMK
68	CITTYLLTGELYN--	NVLTF	GYK
95	CLVELLSSSDV	SDRQK	LQCF
123	VNGVQNDLVST	FPN	YLIS
94	-----VNNSL	FCHS	ANVN
123	-----LAKTH	LLTAL	STQK
93	SDAMHYLL	SKGSI	FEAL
124	TYAFV	DL	LLIN
153	NELFRH	LYTKYL	I
189	NVFEETV	SKKR	KRTI
156	HLPPK	WVQ--	RSSS
186	LKVNDF	KFDK	KQK
217	NVFEETV	SKKR	KRTI
183	HLPPK	WVQ--	RSSS
213	LKVNDF	KFDK	KQK
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	KRTI
185	NVFEETV	SKKR	KRTI
218	HLPPK	WVQ--	RSSS
183	LKVNDF	KFDK	KQK
213	NVFEETV	SKKR	K

FIG. 42
(CONTINUED)

Figure 1

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B.

Sp_Tip1p	219	WNSISISRFSIF	YRSSYKFKQDLYFN	LH	HS	ICD	251
Sc_Est2p	184	N-----	-----	KQFLHKL	NINSS	SFFP	200
Ea_p123	218	NEK--DHFLNN	INVPNWN	NMKSR	TRIF	YCTHFN	248
Sp_Tip1p	252	RNTVHMWLQW	IFPRQFGL	INAFQV	QKLHKV	PL	284
Sc_Est2p	201	-----	YSKILPSS	---S	IKKLT	DLREAIFP	223
Ea_p123	249	R-----	NNQFFKKH	FEVSN	KNNISAM	DRAQTI	275
Sp_Tip1p	285	VS-----	QSTVVPKR	LLKVYPL	IEQTA	KRLHRS	313
Sc_Est2p	224	TN-----	LVKIPQRL	KVRINLT	LQKL	KKRHKRLN	252
Ea_p123	276	FTNIFRFNR	IRKKLKD	KVIEK	AYM	LEKVKDFN	308
Sp_Tip1p	314	LSKVYNHYC	PIYID	-THD	DEKIL	SYSLKPNQ	342
Sc_Est2p	253	YVSLNSIC	PPLEGT	VLDSL	SHSRQ	SPKER	282
Ea_p123	309	FNYLTKSC	PLPENWR	ERKQK	IENT	INKTREK	341
Sp_Tip1p	343	-----	-----	VFAFL	RSIL	VRVFPKLI	359
Sc_Est2p	283	-----	-----	VLKFI	IVIL	QKLPLPQEM	299
Ea_p123	342	SKYYEELF	SYTTDN	KCVTQ	EINE	FFYNILPKDF	374
Sp_Tip1p	360	WGNQRIFEI	ILKIDLE	TFLK	LSRYE	SFSLHYLMS	392
Sc_Est2p	300	FGSKKNKG	IKNLN	LLSL	PLNGY	LPFDSLLK	332
Ea_p123	375	LTG--RNR	KNFQKKV	KYVVE	LKNK	HELHKNLLE	406
Sp_Tip1p	393	NIKISEIEW	LVLGKRS	NAKM	CLSD	FEIKRKQIFA	425
Sc_Est2p	333	KLRLKDFR	WLFI	---D	IWFT	KKHNFENLNQ	362
Ea_p123	407	KINTREIS	WMQVETS	-AKH	FYYFD	HEN-IYVLW	437

FIG. 42

(CONTINUED)

B.			
Sp_Tip1p	426	EF IYWL	YN SFI IPILO
Sc_Est2p	363	CFISWL	FRQLIPKI
Ea_p123	438	KLLRW	IFEDLVSLIRCE
			FFYVITEQQKSY
			KTLY
			470
Sp_Tip1p	459	F	RKD IWKLL
Sc_Est2p	395	F	RHD TWNKLIT
Ea_p123	471	Y	RKNIWDVIMKMS
			ADLKKETLAEV
			QEK EEEV
			503
Sp_Tip1p	492	TQKT	TLPPAVIRL
Sc_Est2p	428	Y	TL SNFNH SKMRI
Ea_p123	504	K	KS LGFAPGKLR
			ILPKK
			534
Sp_Tip1p	523	I	KMG SNK KMLV
Sc_Est2p	461	EEE	-FTIYKENH
Ea_p123	535	N	SD - -RKTTKLT
			TNTKLLNSHLM
			KLK
			554
Sp_Tip1p	553	E	SSGIPFNLE
Sc_Est2p	525	S	FTKIYSP
Ea_p123	565	K	DPFGFAVFN
			YDDVMKKE
			YEEFVCK
			597
Sp_Tip1p	585	Y	FVRIDIK
Sc_Est2p	492	Y	FMKFDVKS
Ea_p123	598	F	EATMDIEK
			YDVS
			616
Sp_Tip1p	617	V	IRKYATIH
Sc_Est2p	558	F	VSRSQYFF
Ea_p123	631	W	IMTAQIL
			KRNKNI
			IVDSKN
			FRKKEM
			KDYFR
			QK
			663

FIG. 42

(CONTINUED)

FIG. 42
(CONTINUED)

FIG. 42

(CONTINUED)

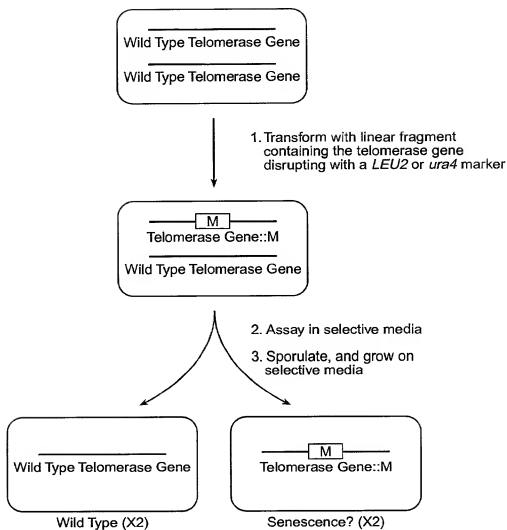
56501

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	860	L A S F A Q V F I D I T H N S K F N S C C N I Y R L G Y S M C M R	882
Sp_Trip1p	773	L N S T N T V L M Q I D H V V K N I S E C - - - - -	793
Sc_Est2p	885	L M N N I T H Y F R K T I T T E D F A N K L T N K L F I S G G Y K	927
Ea_p123			
	883	A Q A Y L K R M K D I F I P Q R M F I T D L L N V I G R K I W K K	915
Sp_Trip1p	904	- - - Y K S A F K D L S I N - - V T Q N M Q F H S F L Q R I I E M	921
Sc_Est2p	928	Y M Q C A K E Y K D H F K K N L A M S S M I D L E V S K I I Y S V	960
Ea_p123			
	916	L A E I L G Y T S R R F L S S A E V K W L F C L G M R D G L K P S	948
Sp_Trip1p	822	T V S G C P I T K C D P L I E Y E V R F I T L N G F L E S L K S N	854
Sc_Est2p	941	T R A F F K Y L V C N I K D T I F G E E H Y P D F F L S T L K H F	993
Ea_p123			
	949	F K Y H P C F E Q L I Y Q F Q S L T D L I K P L R P V L R Q V L F	981
Sp_Trip1p	895	T S - - - - - K F K D N I L L R K E I Q H L Q A Y I Y	877
Sc_Est2p	984	I E I F S - - - T K Y I I E N R V C M I L K A K E A K L K S D Q C	1023
Ea_p123			
	982	L H R R I A D -	988
Sp_Trip1p	878	I Y I H I V N -	884
Sc_Est2p	1024	Q S L I Q Y D A	1031
Ea_p123			

FIG. 42
(CONTINUED)

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(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIG. 43

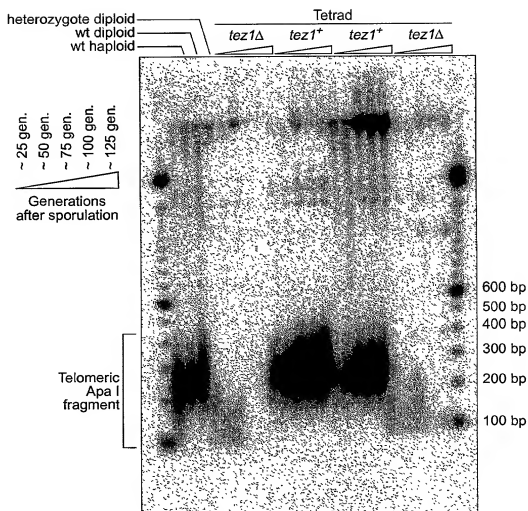


FIG. 45

[illegible]

FIG. 46

1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529
 129 D L V S T F P N Y L I S I L E S K N W Q 148
 1530 CTT TTG TTA GAA AT gtaataaccggttaagatgtgcgacttgcacacttgacaagctgacaagtatag T ATC GGC 1601
 149 L L E I 155
 1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661
 156 S D A M H Y L L S K G S I F E A L P N D 175
 1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721
 176 N Y L Q I S G I F L F K N N V F E E T V 195
 1722 TCA AAA AAA AGA BAG CGA ACC AAT GAA ACA TCC ATT ACT CNA AAT AAA AGC GCC CGC AAA 1781
 196 S K K R K R T I E T S I T Q N N K S A R K 215
 1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841
 216 E V S W N S I S I S R F S I F Y R S S Y 235
 1842 AAG AAG TTT AAG CAA G gtaactaataactgttatccttcataactaatttag AT CTA TAT TTT AAC 1907
 236 K K F K Q D L Y F N 245
 1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967
 246 L H S I C D R N T V H M W L Q W I F P R 265
 1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2037
 266 Q F G L I N A F Q V K Q L H K V I P L V 285
 2038 TCA CAG AGT ACA GTT GTG CCC AAA GGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087
 286 S Q S I V V F K R L L K V Y P L I E Q T 305
 2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147
 306 A K R L H R I S L S K V Y N N H Y C P Y I 325
 2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207
 326 D T H D D E K I L S Y S L K P N Q V F A 345
 2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT ATA TTA ATC TGG GST AAC CAA AGG ATA 2267
 346 F L R S I L V R V F P K L I W G N Q R I 365

FIG. 46

(CONTINUED)

2268 TTT GAG ATA ATA TTA AAA G gattgtataaaattttattaccactaacgattttaccag AC CTC GAA ACT 2336
 366 P E I I L K D L E T 375
 2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396
 376 F L K L S R Y E S F S L H Y L M S N I K 395
 2397 gtaatatgccaattttttaccatttaataacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465
 396 I S E I E W L V L G 405
 2466 AAA AGS TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525
 406 K R S N A K M C L S D F E K R K Q I F A 425
 2526 GAA TTC ATC TAC TCG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TAT 2585
 426 E F I Y W L Y N S F I I P I L Q S F F Y 445
 446 I T E S S D L R N R T V Y F R K D I W K 465
 2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645
 466 L L C R P P I T S M K M E A F E K I N E 485
 2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAA 2705
 486 gatttttaagatatttttgcataagctaatttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775
 2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT ATG AAG AAT ACC TTT CGT CTC ATT ACG 2835
 496 T L P P A V I R L L P K N I F R L I T 515
 2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gattaatttttggctcaatcgaacttttacttcaatctatta 2906
 516 N L R K R F L I K 524
 2907 ttaccag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967
 525 N G S N K K M L V S T N Q T L R P V 542
 2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027
 543 A S I L K H L I N E S S G I P F N L E 562
 3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088
 563 V Y M K L L T F K K D L L K H R M F G 581

FIG 46
(CONTINUED)

3089 tataaatgcgcattccattattatttcgcg G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA 3155
 582 R K K Y F V R I D I
 3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC 3215
 592 K S C Y D R I K Q D L M F R I V K K K L 611
 3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CNT GCA ACA AGT GAC CGA GCT 3275
 612 K D P E F V I R K Y A T I H A T S D R A 631
 3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagttatttttttcattggaatttttaacaa 3343
 632 T K N F V S E A F S Y F 643
 3344 attcttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA 3405
 644 D M V P F E K V V Q L L S M K T 659
 3406 TCA GAT ACT TTG TTT GTT GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT 3465
 660 S D T L P V D F V D Y W T K S S E I F 679
 3466 AAA ATG CTC AAG GAA CNT CTC TCT GGA CAC ATT GTT AAG gataccaattgtgaattgtaataca 3532
 680 K M L K E H L S G H I V K 692
 3533 ctaatgaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 3593
 693 I G N S Q Y L Q K V G I P Q G S 708
 3594 ATT CTG TCA TCT TTT TTG TGT CAT TTG ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653
 709 I L S S F L C H F Y M E D L I D E Y L S 728
 3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 3713
 729 F T K K K G S V L L R V V D D F L F I T 748
 3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgctattcc 3777
 749 V N K K D A K K F L N L S L R G 764
 3778 taagtctaacgcgtgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 3840
 765 F E K H N F S T S L E K T V 778
 3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA 3900
 779 I N F E N S N G I I N N T F F N E S K K 798

FIG. 46

(CONTINUED)

3901 AGA ATG CCA TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960
 799 R M P F F G F S V N M R S L D T L A C 818
 3961 CCT AAA ATT GAT GAA GGC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020
 819 P K I D E A L F N S T S V E L T K H M G 838
 4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgaactgaataatagctgacaataatcag A TCG 4089
 839 K S F F Y K I L R S 848
 4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149
 849 S L A S F A Q V F I D I T H N S K F N S 868
 4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209
 869 C C N I Y R L G Y S M C M R A Q A Y L K 888
 4210 AGG ATG AGG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtagtaactattttaactaga 4274
 889 R M K D I F I P Q R M F I T D 903
 4275 aaagtcattaataaccttag AT CTT TTG AAT GUT ATT GGA AGA AAA AAT TGG AAA AAG TTG GCC 4339
 904 L L N V I G R K I W K K L A 917
 4340 GRA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgc 4401
 916 E I L G Y T S R R F L S S A E V K W 935
 4402 ggctcgcgagacttcagcaatattgacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4466
 936 L F C L G M R D G L K 946
 4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528
 947 P S F K Y H P C F E Q L I Y Q F Q S L I 966
 4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CCA CAG GTG TTA TTT TTA CXT AGA ATA 4588
 967 D L I K P L R P V L R Q V L F L H R R I 986
 4589 GCT GAT TAA tgcattttcaattattatatatacaactccttattattgggtgcttaacaataattattactaagtata 4665
 987 A D 989

FIG. 46
(CONTINUED)

4666 gctgacccccaaagcaagcctactataggattctctgaatgaataaattaatccttattgaattttgactgaattgct 4745
 4667 ttactctatattgaagttgagttctggaactactgcccacatgcccattaaacgagtggttaaac 4825
 4668 tttctctatattgaagttgagttctggaactactgcccacatgcccattaaacgagtggttaaac 4905
 4669 atcgaagaagcgaagattctctcttcaatttgatcaggaaggggtttctctataatgaataatccgcgacta 4985
 4670 atcgaagaagcgaagattctctcttcaatttgatcaggaaggggtttctctataatgaataatccgcgacta 4985
 4671 gtgagaagaagcgaagattctctcttcaatttgatcaggaaggggtttctctataatgaataatccgcgacta 5065
 4672 gtgagaagaagcgaagattctctcttcaatttgatcaggaaggggtttctctataatgaataatccgcgacta 5065
 4673 cccaggtttatccatgggtgcccggcgttgcctactgagacgaagaactaaagttatggttgacccgaatttggtaaaagc 5145
 4674 atgtctctataaagtttggtttttctgactcaatttgcattgggtgaaagaaatagtgtaagccattatctggat 5145
 4675 tccgaataatgccaatttctgtgttctcctcaagcgaagttctaaagaaacttatgaagcttatgagcttcaaaaactcc 5225
 4676 tccgtgattaaaggaagattctccaccgatgaggaatggatagcttatccagctctgaggaagacctaatattttgc 5305
 4677 tccgtgattaaaggaagattctccaccgatgaggaatggatagcttatccagctctgaggaagacctaatattttgc 5385
 4678 aaaaagaataatcatcttggagagacatctcttgatgaatccagatcggaaggtatctccagcggaatccttgatgccaata 5465
 4679 acttctattctgaaatgtatggctctactgtcgtctcgaactctctgtagcttcaagcagttaatgaccaaaaggtacc 5544

FIG. 46

(CONTINUED)

1
 met ser val tyr val val glu leu leu
 GCCAAGTTCCTGCACTGGCTG ATG AGT GTG TAC GTC GTC GAG CTG CTC

10
 arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
 AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

20
 leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
 CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

30
 gly ile arg gln his leu lys arg val gln leu arg glu leu ser
 GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

40
 glu ala glu val arg gln his arg glu ala arg pro ala leu leu
 GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

50
 thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
 ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

60
 ile val asn met asp tyr val val gly ala arg thr phe arg arg
 ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

70
 glu lys ala glu arg leu thr ser arg val lys ala leu phe
 GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

80
 ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
 AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

90
 ala ser val leu gly leu asp asp ile his arg ala trp arg thr
 GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

100
 phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
 TTC GTG CTG CGT GTG CGG GCC CAG GAC CGG CCT GAG CTG TAC

110
 phe val lys val asp val thr gly ala tyr asp thr ile pro gln
 TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

120
 asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
 GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC AAA CCC CAG AAC

130
 thr tyr cys val arg arg tyr ala val val gln lys ala ala met
 ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG

140
 150
 160
 170
 180
 190
 200

FIG. 47

210
 gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
 GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC
 220
 gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
 CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC
 240
 leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
 CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG
 250
 arg asp gly leu leu leu arg leu val asp asp phe leu leu val
 CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG
 270
 thr pro his leu thr his ala lys thr phe leu arg thr leu val
 ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC
 280
 arg gly val pro glu tyr gly cys val val asn leu arg lys thr
 CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA
 290
 val val asn phe pro val glu asp glu ala leu gly gly thr ala
 GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CCG GGT GGC ACG GCT
 300
 phe val gln met pro ala his gly leu phe pro trp cys gly leu
 TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG
 310
 leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
 CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC
 320
 tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
 TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC
 330
 phe lys ala gly arg asn met arg arg lys leu phe gly val leu
 TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG
 340
 arg leu lys cys his ser leu phe leu asp leu gln val asn ser
 CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC
 350
 leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
 CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG
 360
 ala tyr arg phe his ala cys val leu gln leu pro phe his gln
 GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

FIG. 47
(CONTINUED)

420
 gln val trp lys asn pro his phe ser cys ala ser ser leu thr
 CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

 430
 arg leu pro leu leu leu his pro glu ser 440
 CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

 450
 val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
 GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

 460
 arg ala val ala val pro pro ser ile pro 470
 CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

 480
 thr pro cys his leu arg ala thr pro gly val thr gln asp ser
 ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

 490
 pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
 CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

 510
 pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
 CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

 520
 his pro gly leu met ala thr arg pro gln 530
 CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

 540
 thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
 ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

 550
 arg gly gly pro his pro gly leu his arg 560
 AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

 564
 OP
 TGA GTGAGTGTGTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC
 CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC
 AGGCTGGCGTTCCGTCCACCCAGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACT
 CCCACATAGGAATAGTCCATCCCCAGATTGCGCATTTGTTACCCCTTCGCCCTGCCTTCC
 TTTGCTTCCACCCCCACCATTCAGSTGGAGACCTGAGAAGGACCTGGGAGCTTTGGG
 AATTGGAGTGACCAAGGTGTGCTCCTGTACACAGGCGAGGACCTGCACCTGGATGGGG
 GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATAGATT
 TTTCAAGTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 47
(CONTINUED)

Motif -1
 Ep p123 ...LVVSLIRCFYVTEQOKSYSKT...
 Sp Tez1 ...FIIPILQSFYITESSDLRNRT...
 Sc Est2 ...LIPKLIOTFFYCTEISSVTIV...
 Hs TCP1 ...YVVELLSFFYVTETTFQKNRL...
 consensus FFY TE

Motif 0
 Ep p123 ...KSLGFAPGKLRLLPKKT--TFRPIMTFNKKIV...
 Sp Tez1 ...QKTTLPPAVIRLLPKKN--TFRLITNLKRFL...
 Sc Est2 ...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...
 Hs TCP1 ...ARPALLTSRLRFIPKPD--GLRPIVNMDDYVVG...
 consensus R PK R I

Motif A
 Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...
 Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
 Sc Est2 ...PELYFMKFDVKSCYDISIPRMECMRIK...
 Hs TCP1 ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
 consensus F D YD

Motif B
 Ep p123 ...NGKFKYQTKGIPQGLCVSSILSSFYYA...
 Sp Tez1 ...GNSQYLQKVGIPQGSILSSFLCHFMYE...
 Sc Est2 ...EDKCYIREDGLFQGSLSAPIVDLVYD...
 Hs TCP1 ...RATSYVQCGIPQGSILSTLLCSLCYG...
 consensus G QG S

Motif C
 Ep p123 ...PNVNLLMRLTDDYLLITTQENN...
 Sp Tez1 ...KKGSVLLRVVDDFLFITVNKKD...
 Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...
 Hs TCP1 ...RRDGLLLRLVDDFLVLTPHLTH...
 consensus DD L

Motif D
 Ep p123 ...NVSRENGFKFMKKL...
 Sp Tez1 ...LNLSLRGFEKHNST...
 Sc Est2 ...KKLAMGGFOKYNKA...
 Hs TCP1 ...LRTLVRGVPEYGCVV...
 consensus G

FIG. 48

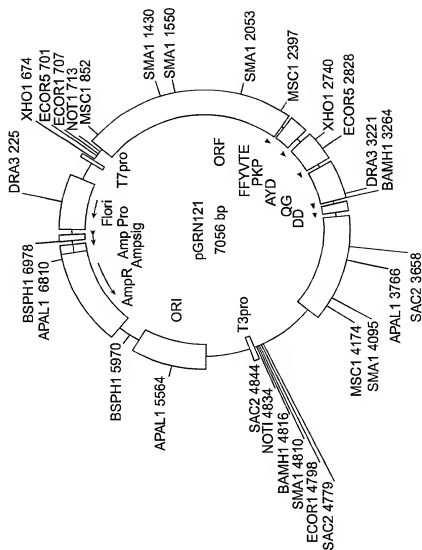


FIG. 49

1 GCACGCGTGC GTCTCTGCTGC GCACGCTGGGA AGCCCTTGGCC CGGGCCACCC
 51 CCGCGATGCC GCGCGCTCCC CGTGCAGAG CCGTGGGCTC CCTGCTGGCG
 101 AGCCACTACC GCGAGGTGCT GCGCTTGCGC ACGTTCGTGC GCGCGCTGGG
 151 GCCCCAGGGC TGGCGGCTGG TGCAAGCGGG GGAACCGGGC GCTTTCGGCG
 201 CGNTGGTGGC CCANTCGNTG GTGTGCGTGC CTTGGGANGN ANGGCNGCCG
 251 CCGCGCGGCC CTTCTTTCGG CCAGGTGTGC TGCTTGAANG ANCTGGTGGC
 301 CCGAGTGTGC CANANGCTGT GCGCAGCGGG CGCAANAAC GTGCTGGGCT
 351 TCGGCTTGGC GTTCTTGGAC GGGGCCCGCG GGGGCCCTTC CGAGGCTTTC
 401 ACCACAGCGC TGGCAGCTTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG
 451 GGGGAGCGGG GCGTGGGGGC TGCTGTGCG CCGGTGGGC GACGACGTGC
 501 TGCTTACCTT GCTGGCAGCG TGCGCGTNTT TGTGCTGGT GGNTCCCGAC
 551 TGCGCTTACC ANGTGTGCGG GCGCGCGCTG TACCAGCTCG GCGCTGCNAC
 601 TCAGGCCCGG CCCCAGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC
 651 CAACGGGCGT GGAACCATAG CGTCAGGGAG GCGGGGGTCC CCTTGGGCTG
 701 CCAGCCCGGG GTGCGAGGAG GCGCGGGGGC AGTGCACGCC GAAGTCTGCC
 751 GTTGCCCAAG AGGCCAGGC GTGGCGCTGC CCTGAGCCG GAGCGGACGC
 801 CCCTTGGGCA GGGGTCTGCG GCCCACCCTG CAGGAGCGCC TGGACCGGAT
 851 GACCGTGGTT TCTGTGTGGT GTCACTTGCC AGACCCGCGC AAGAAGCCAC
 901 CTCTTTGGAG GGTGCGCTCT CTGGCACGGC CCACTCCCAAC CCATCCGTGT
 951 GCGGCCAGCA CCAAGCGGGC CCCCATTCCA CATCGCGGCC ACCAGCTGCT
 1001 GGGCACCGCC TTGTCCCCCG GTGTACGCGC AGACCAAGCA CTTCCTCTAC
 1051 TCTCAGGCG ACAAGNACAC TGGNCCCTC CTTCCTACTC AATATATCTG
 1101 AGGCCACGCC TGACTGGGCT TCGGGAGGTT CGTGAGACA NTCTTCTGTG
 1151 TTCCAGGCTT TGGATGCCAG GATTCCCGCG AGGTTCGCCG GCCTCCGCCA
 1201 GCGNACTGCG CAAATGCGGC CCTGTCTTCT GAGCTGCTTT GGAACCCAGC
 1251 CGCAGTGCCC CTACGGGGTG TTCTCAAGA CGCACTGCCC GTGCGAGCTG
 1301 GCGGTCACCC CAGCAGCGCG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
 1351 TGTGGCGGCC CCGGAGGAGG AGGAACAACG ACCCCGTCG CTTGGTGAGC
 1401 CTGTCTCCGC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGGGGCG
 1451 CTGCTCGCGC CGGCTGGTGC CCCCAGGCTT CTGGGGCTCC AGGCACAAGC
 1501 AACCGCGCTT CCTCAGGAAC ACCAAGAAAT TCATCTCCCT GGGGAAGCAT
 1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGGCGGACTG
 1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCGCGAGAGC
 1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAAT TCCTGCACTG GCTGTATAGT
 1701 GTGTACGTCG TCGAGCTGCT CAGGCTTTTC TTTTATGTCA CGGAGACCAC
 1751 GTTTCAAAG AACAGGCTCT TTTTCTAACG GAAGAGTGTG TGGAGCAAGT
 1801 TGCAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GTGCGGGAGC
 1851 CTGTCCGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
 1901 GACGTCCAGA CTCGCTTCA TCCCACAAGC TGACGGGGCTG CGGCGGATGG
 1951 TGAACATGGA CTACGTCTGT GAGGCCAGAA CGTTCCGAG AGAAAAGAGG
 2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTCCAGC TGCTCAACTA
 2051 CGAGCGGGCG CGGCGCCCCG GCCTCTGGG CGCCTCTGTG CTGGGCTTGG
 2101 ACGATATCCA CAGGGCTTGG CGCACTTTCG TGCTGCGTGT GCGGGCCGAG
 2151 GACCCCGCCG CTGAGCTGTA CTTTGTCAAG GTGATGTGA CGGGCGGTA
 2201 CGACACCATC CCCCAGGACA GGCTCACGGA GTGCATCGCC AGCATCATCA
 2251 AACCCAGAA CACGTACTGC GTGCGTCGTT ATGCGTGGT CCAGAAAGGCC
 2301 GCCCATGGGC ACGTCCGCAA GGCTTCAAG AGCCACGTCT CTACCTTGAC
 2351 AGACCTCCAG CGGTACATGC GACAGTTGCT GGCTCACCTG CAGGANAACA
 2401 GCCCGCTGAG GGAATGCCGT GTCATCGAGC AGAGCTCTCT CCTGAATGAG
 2451 GCCAGCAGTG GCTCTTCGA GCTTCTCCTA CGCTTCATGT GCCACCAGCG

FIG. 50

2501 CGTGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCGCGAGG
 2551 GCTCCATCCT CTCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG
 2601 AACAAAGCTGT TTGCGGGAT TCGGCGGGAC GGGCTGCTCC TGCCTTTGGT
 2651 GGATGATTTT TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC
 2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACCTG
 2751 CGGAAGACAG TGGTGAACCT CCTGTAGAA GACGAGGCC TGGGTGGCAC
 2801 GGCTTTTGT T CAGATGCCGG CCCACGGCCT ATTCCCTGG TCGGCGCTGC
 2851 TGCTGGATAC CCGACCCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC
 2901 CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGCTGG
 2951 GAGGAACATG CGTCGCAAA TCTTTGGGGT CTTCGCGCTG AAGTGTCACA
 3001 GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC
 3051 ATCTACAAGA TCCTCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT
 3101 GCAGCTCCCA TTTTCATCAGC AAGTTTGGAA GAACCCACA TTTTTCCTGC
 3151 GCGTCATCTC TGACACGGCC TCCTCTGCT ACTCCATCCT GAAAGCCAAG
 3201 AACGCAGGGA TGTGCTGGG GGCCAAGGGC GCCGCGGCC CTCTGCCCTC
 3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCTGTCTC AAGCTGACTC
 3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCAG
 3351 ACGCAGCTGA GTCGGAAGCT CCCGGGACG ACGCTGACTG CCTGGAGGC
 3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC GGCCTGTAC
 3451 GGCCACCCGC CCAAGCCAG GCGGAGAGCA GACACCAACA GCGGCGCCG
 3501 GCGGGGCTCT ACGTCCAGG GAGGGAGGGG CGGCCACAC CAGGCGCCG
 3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT
 3601 CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA
 3651 GGGCTGAGTG TCCAGCACAC CTGCGTCTT CACTTCCCA CAGGCTGGCG
 3701 CTCGGCTCCA CCCAGGGCC AGCTTTCTT CACGAGAGC CCGCTTCCA
 3751 CTCCCACAT AGGAATAGTC CATCCCCAGA TTGCCATTG TTCACCCCTC
 3801 GCCCTGCCCT CTTTTCCTT CCACCCCA CACAGGAGT GAGACCTGA
 3851 GAAGGACCTT GGGAGCTCTG GGAATTTGGA GTGACCAAG GTGTGCCCTG
 3901 TACACAGCG AGGACCTGTC ACCTGATGG GGGTCCCTGT GGTCAAATT
 3951 GGGGGGAGGT GCTGTGGAG TAAATATCTG AATATATGAG TTTTTCAGTT
 4001 TTGAAAAAAA AAAAAAAA AAAAAAAA

FIG. 50
(CONTINUED)

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GCAGCGCTGCGTCTGCTGCGCACTGGGAAGCCCTGGCCCGGCCACCCCGCGATGCC
 1 -----+-----+-----+-----+-----+ 60
 CGTGCAGCAGCAGGACGACGCGTGCACCTTCGCGACCGGGCCGCTGGGGCGCTACGG
 a A A L R P A A H V G S P G P G H P R D A -
 b R C V L L R T W E A L A P A T P A M P -
 c S A A S C C A R G K P W P R P P P R C R -
 GCGCGTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCACTACCGGAGGTGCT
 61 -----+-----+-----+-----+-----+ 120
 CGCGCAGGGGGCGACGGCTCGGCACGCGAGGACGACGCGTTCGGTATGCGCTCCACGA
 a A R S P L P S R A L P A A Q P L P R G A -
 b R A P R C R A V R S L L R S H Y R E V L -
 c A L P A A E P C A P C C A A T T A R C -
 GCGCGTGGCCACGTTCTGTCGGGGCGCTGGGGCCCGAGGGCTGGCGGCTGGTGCGAGCGCGG
 121 -----+-----+-----+-----+-----+ 180
 CGGGACCGGTGCAAGCAGCGCCGCGGACCCCGGGGTCCCGACCGCCGACCACTGCGCGCC
 a A A G H V R A A P G A P Q G L A A G A A R -
 b P L A T F V R R L G P Q G W R L V Q R G -
 c R W P R S C G A W G P R A G G W C S A G -
 GGACCCGGCGGCTTTCGCGCGNTGGTGGCCANTGNTGGTGTGCGTGCCCTGGGANGN
 181 -----+-----+-----+-----+-----+ 240
 CCTGGCGCGCAAAAGCGCGGNACACCGGGTACGACACCAAGCAGCGGACCCCTCN
 a G P G G F P R ? G G P ? ? G V R A L G ? -
 b D P A A F P R A ? V A ? C ? V C V P W ? ? -
 c T R R L S A R W W P ? A W C A C P G ? ? -
 ANGGCNGCCCCCGCGCCCTCCTTCGCCAGGTTCCTCGCTGAANGANTGTTGGC
 241 -----+-----+-----+-----+-----+ 300
 TNCNGCGGGGGCGCGCGGGGAGGAAGCGGTCCACAGGACGGACTTNTGACCAACCG
 a ? A A P R R P L L P P G V L P E ? ? G G -
 b ? ? P P A A P S F R Q V S C L ? ? L V A -
 c G ? P P P P P P S A R C P A * ? ? W W P -
 CCGAGTGTGCANANGCTGTGCGANCGCGGCCGAANAACGTGTGCGCTTCGGCTTCGC
 301 -----+-----+-----+-----+-----+ 360
 GGCTCAGGACGTTNTGACACGCTNGCGCGCGCTTNTGACGACCGGAAGCGGAAGCG
 a P S A A ? A V R ? R R E ? N V A G L R L R -
 b R V L ? ? L C ? R G A ? R V L A F G P A -
 c E C C ? ? C A ? A A R ? T C W P S A S R -
 GCTGTGAGCGGGCGCGGGGGCCCCCGAGGCGCTTCACACAGCGGTGCGCAGCTA
 361 -----+-----+-----+-----+-----+ 420
 CGACGACTGCCCCGGCGCCCCCGGGGGGCTCCGGAAGTGGTGCACGCGTCCGAT
 a A A G R G P R G P P R G L H H Q R A Q L -
 b L L D G A R G G P P P E A F T T S V R S Y -
 c C W T G P A G A P P R P S P P A C A A T -
 CTTGCCCAACCGGTGACCGACGCACTGCGGGGAGCGGGCGTGGGGGCTGCTGCTGG
 421 -----+-----+-----+-----+-----+ 480
 GGACGGTTGTGCCACTGGTGCCTGACGCCCTTCGCCCGACCCCGACGACGACGC
 a P A Q H G D R R T A G E R G V G A A A A -
 b L P N T V T D A L R G S G A W G L L L R -
 c C P T R * P T H C G G A G R G G C C A -

FIG. 51

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a      P R G R R R A G S P A G T L R ? ? C A G -
b      R V G D D V L V H L L A R C A ? F V L V -
c      A W A T T C W F T C W H A A R ? L C W W -

541  G G N T C C C A G T G C G C T A C C A N G T G T G C G G C C C G C T G T A C C A G T C G C G C T G C N A C
      C C N A G G G T C G A C G C G A T G G T N C A C A G C C C G G C G G G A C A T G S T C G A G C C G A C G N T G

a      G S Q L R L P ? V R A A A V P A R R C ? -
b      ? P S C A Y ? V C G P P L Y Q L G A A T -
c      ? P A A P T ? C A G R R C T S S A L ? L -

601  T C A G C C C G G C C C C C C A C A C G C T A N T G G A C C C G A A N G C G T C T G G G A T C C A A C G G G C C T
      A G T C C G G G C C G G G G C G T G T G C G A T N A C T G G G C T T N C G C A G A C C C T A G S T T G C C G G A

a      S G P A P A T R ? W T R ? R L G S N G P -
b      Q A R P P P H A ? G P E ? V W D P T G L -
c      R P G P R H T L ? D P ? A S G I Q R A W -

661  G G A A C C A T A G C G T C A G G A G G C C G G G T C C C C T G G G C T C C A G C C C C G G T C G A G G A G
      C C T T G G T A T C G A G T C C T C G G C C C C A G G G G A C C G A C G S T C G G G C C C A C G C T C C T C

a      G T I A S G R P G S P W A A S P G C E E -
b      E P * R Q G G R G P P L G L P A P G A R R -
c      N H S V R E A G V P L G C Q P R V R G G -

721  G C G C G G G C A G T G C C A G C C A A G T C T G C C G T T G C C A G A G G C C C A G C G T G G C G T G C
      C G C G C C C C G T C A C G G T C G G C T T C A G A C G G C A A C G G G T T C T C G G G T C C G A C C C G A C G

a      A R G Q C Q P K S A V A Q E A Q A W R C -
b      R G G S A S R S L P L P K R P P R R G A A -
c      A G A V P A E V C R C P R G P G V A L P -

781  C C C T G A G C C G A G C G G A C C C C G T T G G G C A G G G T C C T G G G C C C A C C C G G C A G A C G C C
      G G G A C T C G G C C T C G C T G C G G C A A C C G T C C C A G A C C C G G T G G G C C G T C C T G C G G

a      P * A G A D A R W A G V L G P P G Q D A -
b      P E P E R T P V G Q G S W A H P G R T P -
c      L S R S G R P L G R G P G P T R A G R L -

841  T G G A C C G A G T G A C C G T G T T C T G T G T G T G T C A C C T G C C A G A C C C C G A A G A G C C A C
      A C C T G G C T C A C T G G C A C C A A G A C A C A C A C A G T G A C G G T C T G G G C G C T T C T C G G T G

a      W T E * P W F L C G V T C Q T R R R S H -
b      G P S D R G F C V V S P A R P A E E A T -
c      D R V T V V S V W C H L P D P P K K P P -

901  C T C T T T G G A G G T G C G C T C T C T G G C A C G C C C A C T C C C A C C C A T C C G T G G G C C G C A C A
      G A G A A C C T C C C A C G C G A G A C C S T G C G C G T G A G G T G G T A G G C A C C C G C G T C G T

a      L P G G C A L W H A P L P P I R G P P A -
b      S L E G A L S G T R H S H S P S V G R Q H -
c      L W R V R S L A R A T P T H P W A A S T -

961  C C A C G C G G C C C C C A C C A C A C T C G C G C C A C C A C G T C C T G G S A C A C G C T T G T C C C C G
      G T G C G C C C G G G G T A G T G T A G C C C G T G T G C A G G A C C C T G T C G S A A C A G G G G C

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FIG. 51
(CONTINUED)

a P R G P P I H I A A T T S W D T P C P P -
 b H A G P P S T S R P P R P G T R L V P R -
 c T R A P H P H R G H V L G H A L S P G -
 GTGTAGCGCGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAGNACACTGCGNCCCTC
 1021 CACATGCGGCTCTGGTTCTGGAAGGAGATGAGGAGTCCGCTGTTCTNTGTGAGCGNGGGAG
 V Y A E T K H F L Y S S G D K ? T A ? L -
 a C T P R P S T S S T P Q A T ? T L R P S -
 b V R R D Q A L P L L L R R Q ? H C ? P P -
 c CTTCTACTCAATATATCTGAGGCCAGCCTGACTGGCGTTCGGGAGGTTCTGTGAGACA
 1081 GAAGGATGAGTTATATAGACTCCGGGTCGGACTGACCGCAAGCCCTCCAGCACCTCTGT
 L P T Q Y I * G P A * L A F G R F V E T -
 a F L L N I S E A Q P D W R S G G S W R ? -
 b S Y S I Y L R P S L T G V R E V R G D ? -
 c NTCITTTCTGGTTCAGGCCCTTGGATGCCAGGATTCGCCGAGGTTGCCCGCCTGCCCA
 1141 NAGAAAGACCAAGGTCGGAACTACGGTCTAAGGGGCTCCAACGGGGCGGACGGGT
 ? F L V P G L G C Q D S P Q V A P P A P -
 a S P W F Q A L D A R I P R R L P R L P O -
 b L S G S R P W M P G F P A G C P A C F S -
 c GCGNTACTGGCAAAATGCGGCCCTGTTTCTTGGAGCTGCTTGGGAACACGCGCAGTGCCTC
 1201 CCGNATGACCGTTTACGCCGGGGAACAAGACTCGACGAACCTTGGTGGCGGTCAAGG
 A ? L A N A A P V S G A A W E P R A V P -
 a R Y W Q M R P L F L E L L G N H A Q C P -
 b ? T G K C G P C F W S C L G T T R S A P -
 c CTACGGGGTGTCTCTCAAGACGCACTGCCCGCTCGAGCTGCGGTCAACCCACAGCAGCGG
 1261 GATGCCCCACAAGGAGTTCGTGTGACGGGCGAGCTCGACGCCAGTGGGGTGTGCGGC
 L R G V P Q D A L P A A S C G H P S S R -
 a Y G V F L K T H C P L R A A V T P A A G -
 b T G C S S R R T A R C E L R S P Q Q P V -
 c TGTCTGTGCCCGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCGGAGGAGGAAACAG
 1321 ACAGACACGGGCCCTCTTCTGGGGTCCCGAGACACCGCGGGGGCTCTCTCTCTGTGTGTC
 C L C P G E A P G L C G G P R G G G T Q -
 a V C A R E K P Q G S V A A P E E E E H R -
 b S V P G R S P R A L W R P P R R R N T D -
 c ACCCCCGTCGCTGTGTCAGCTGCTCCGCCAGCACAGCAGCCCTTGGCAGGTGTGACGGCT
 1381 TGGGGCAGCGGACCACTGTGACGAGAGCGGTGTGTGTGTGCGGACCGGTCCACATGCCGA
 T P V A W C S C S A S T A A P G R C T A -
 a P P S P G A A A P P A Q O P L A G V R L -
 b P R R L V Q L L R Q H S S P W Q V Y G F -
 c TGTGCGGGCTGCCTGCGCGGCTGTGTGCCCGCAGGCTCTGGGGCTCAGGCACAAAG
 1441 AGCACGCCCGGACGGAGCGGCGGACCAAGGGGGTCCGGAGACCCGAGGTCTGTGTGTC

 FIG. 51
 (CONTINUED)

a S C G P A C A G W C P Q A S G A P G T T -
 b R A G L P A P A G A P R P L G L Q A Q R -
 c V R A C L R R L V P P G L W G S R H N E -
 AACGCCGCTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCT
 1501 -----+----- 1560
 TTGGCGCGAAGGAGTCTTGTGGTTCTTCAAGTAGAGGGACCCCTTCTGACGGTTCGAGA
 a N A A S S G T P R S S S P W G S M P S S -
 b T P L P Q E H Q E V H L P G E A C Q A L -
 c R R F L R N T K K F I S L G K H A K L S -
 CGCTGCAGGAGCTGACGTGGAAATGAGOGTGCAGGAGCTGCCTTGGCTGCAGGAGGCC
 1561 -----+----- 1620
 GCGACGCTCTCGACTGCACCTTCTACTCGCAGCCCTGACGCGAACCAGGOGTCTCTCGG
 a R C R S * R G R * A C G T A L G C A G A -
 b A A G A D V E D E R A G L R L A A Q E P -
 c L Q E L T W K M S V R D C A W L R R S P -
 CAGGGTGGCTGTGTTCGCGCCGAGAGCACCGTCTGCCTGAGGAGATCCTGGCCCAAGT
 1621 -----+----- 1680
 GTCCCAACCGACACAGGCCGCGCTCTGTTGCGAGAGCTCCTCTAGGACCGGTTC
 a Q G L A V F R P Q S T V C V R R S W P S -
 b R G W L C S G R R A P S A * G D P G Q V -
 c G V G C V P A A E H R L R E E I L A K F -
 TCCTGCAGTGGCTGATGAGTGTGTAGCTGTCGAGCTGCTCAGGTCTTCTTTATGTCA
 1681 -----+----- 1740
 AGGACGTGACCGACTACTCACATGCAGCAGCTCGACGAGTCCAGAAAGAAATACAGT
 a S C T G * * V C T S S S S C S G L S F M S -
 b P A L A D E C V R R R R A A Q V F L L C H -
 c L H W L M S V Y V V E L L R S F F Y V T -
 CGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGAGCAAGT
 1741 -----+----- 1800
 GCCTCTGGTGCAAAGTTTCTGTGCGAGAAAAGATGGCTTCTCACAGACCTCGTTCA
 a R R P R F K R T G S F S T G R V S G A S -
 b G D H V S K E Q A L F L P E E C L E Q V -
 c E T T F Q K N R L F F Y R K S V W S K L -
 TGCAAGCATTTGGAATCAGACAGCACTGAAAGAGGTTGACGCTGCGGAGAGCTGCGGAG
 1801 -----+----- 1860
 AGCTTTCGTAACTTAGTCTGTGTGTAACCTTCTCCACGTGACGCGCTCGACAGCCTTC
 a C K A L E S D S T * R G C S C G S C R K -
 b A K H W N Q T A L E E G A A A G A V G S -
 c Q S I G I R Q H L K R V Q L R E L S E A -
 CAGAGGTGAGGAGCATGCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCGCTTCA
 1861 -----+----- 1920
 GTCTCCAGTCCGTGAGCCCTTGGTCCGCGCGGAGCACTGACGCTGAGGCGAAGT
 a Q R S G S I G K P G P P C * R P D S A S -
 b R G Q A A S G S Q A R P A D V Q T P L H -
 c E V R Q H R E A R P A L L T S R L R F I -
 TCCCAAGCCTGACGCGCTGCGGCCGATTGTGAACATGGACTACGTGTTGGGAGCCAGAA
 1921 -----+----- 1980
 AGGGGTTCGAGTGCAGGAGCGCCGCTAACACTGTGTACTGTATGACGACCCCTGCTCTCT

 FIG. 51
 (CONTINUED)

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a   S P S L T G C G R L * T W T T S W E P E -
b   P Q A * R A A A D C E H G L R R G S Q N -
c   P K P D G L R P I V N M D Y V V G A R T -

CGTTCGCGAGAGAAAGAGGGCGAGCGTCTCACCTCGAGGGTGAAGGCACGTGTCAGCG
1981 -----+-----+-----+-----+-----+
GCAAGGCGTCTCTTTTCTCCGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTGGC

a   R S A E K R G P S V S P R G * R H C S A -
b   V P Q R K E G R A S H L E G E G T V Q R -
c   F R R E K R A E R L T S R V K A L F S V -

TGCTCAACTACGAGCGGGCGCGCGCCCGGCGCTCCTGGGCGCCTCTGTGCTGGGCGCTGG
2041 -----+-----+-----+-----+-----+
ACGAGTGTGATGCTGCGCCGCGCGCGCGGGCCGGAGGACCCGCGGAGACACGACCCGAGCC

a   C S T T S G R G A P A S W A P L C W A W -
b   A Q L R R A G A A P R P P G R L C A G P G -
c   L N Y E R A R R R F G L L G A S V L G L D -

ACGATATCCACAGGGCGCTGGCGCACCTTCGTGCTGTGCGGGCCAGGACCCCGCCG
2101 -----+-----+-----+-----+-----+
TGCTATAGGTGTCCCGGACCGCGTGGAGCACGACGACACGCGCCGGTCTGTGGCGGGCG

a   T I S T G P G A P S C C V C G P R T R R -
b   R Y P Q G L A H L R A A C A G P G P A A -
c   D I H R A W R T F V L R V R A Q D P P P -

CTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGGTACGACACCATCCCCAGGAGA
2161 -----+-----+-----+-----+-----+
GACTCGACATGAACAGTTCACCTACACTGCGCGCGCATGCTGTGGTAGGGGGTCTGT

a   L S C T L S R W M * R A R T T P S P R T -
b   * A V L C Q G G C D G R V R H H P P G Q -
c   E L Y F V K V D V T G A Y D T I P Q D R -

GGCTCACGGAGGTTCATCGCCAGCATCATCAAAACCCAGAAACGTAAGTGTGGTGTGGT
2221 -----+-----+-----+-----+-----+
CGAGTGTGCTCCAGTAGCGTCTGTAGTGTGGGGTCTTGTGCATGACGACGACGCCA

a   G S R R S S P A S S N P R T R T A C V G -
b   A H G G H R Q H H Q T P E H V L R A S V -
c   L T E V I A S I I K P Q N T Y C V R R Y -

ATGCCGTGGTCCAGAGGGCCGCCATGGGCAGTTCGCAAGGCCCTTAAGAGCCACGTCT
2281 -----+-----+-----+-----+-----+
TACGGCACAGGTCTTTCGGCGGGTACCGTGCAGGCGTTCGGAAGTTCTCGTGCAGAG

a   M P W S R R P P M G T S A R P S R A T S -
b   C R G P E G R P W A R P Q G L Q E P R L -
c   A V V Q K A A H G H V R K A F K S H V S -

CTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGANAACA
2341 -----+-----+-----+-----+-----+
GATGGAACTGTCTGGAGGTGCGCATGTACGCTGTCAAGCACCGAGTGGACGCTCTTGTGT

a   L P * Q T S S R T C D S S W L T C R ? T -
b   Y L D R P P A V H A T V R G S P A G ? Q -
c   T L T D L Q P Y M R Q F V A H L Q ? N S -

GCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCACGAGTG
2401 -----+-----+-----+-----+-----+
CGGGCGACTCCCTACGGCAGTAGTGTCTCTCGAGGAGGAGCTTACTCGGTGTGTAC

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FIG. 51
(CONTINUED)

FIG. 51
(CONTINUED)

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a T T P A M P G P P S E P V S P S T A A -
 b R L L Q L C P D L H Q S Q S H L Q P R L -
 c D Y S S Y A R T S I R A S L T F N R G F -
 TCACGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGCGCTGAAGTGTACA
 2941 -----+-----+-----+-----+-----+ 3000
 AGTTTCGAGCCCTCCTTGTAGCGAGCGTTTGAGAAACCCGAGAAGCCGACTTCACAGTGT
 a S R L G G T C V A N S L G S C G * S V T -
 b Q G W E E H A S Q T L W G L A A E V S Q -
 c K A G R N M R R K L F G V L R L K C H S -
 GCCTGTTCTGGATTGTCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGA
 3001 -----+-----+-----+-----+-----+ 3060
 CGGACAAAGACCTAAACGTCCACTGTGTCGGAGGTCTGCCACACGTTGGTTGTAGATGTTCT
 a A C F W I C R * T A S R R C A P T S T R -
 b P V S G F A G E Q P P D G V H Q H L Q D -
 c L P L D L Q V N S L Q T V C T N I Y K I -
 TCCTCCTGCTGCAGGCGTACAGGTTTCAAGCATGTGTGCTGCAGCTCCCATTTTCATCAGC
 3061 -----+-----+-----+-----+-----+ 3120
 AGGAGGACGAGCTCGCATGTTCCAAAGTCGCTACACAGACGTCGAGGGTAAGATAGTGG
 a S S C C R R T G P T H V C C S S H F I S -
 b P P A A G V Q V S R M C A A P I S S A -
 c L L L Q A Y R F H A C V L Q L P P H Q Q -
 AAGTTTGAAGAACCACATTTTTCTCGCGCTCATCTCTGACACGGCTCCCTCTGCT
 3121 -----+-----+-----+-----+-----+ 3180
 TTCAAACCTTCTTGGGGTGTAAAAAGGAGCGCAGTAGAGACTGTGCCGGAGGGAGACGA
 a K F G R T P H F S C A S S L T R P P S A -
 b S L E E P H I F P A R H L * H G L P L L -
 c V W K N P T F P L R V I S D T A S L C Y -
 ACTCCATCTGAAGGCCAAGAACGACGAGGATGTGCTGGGGGCCAAGGGCGCCGCGCGCC
 3181 -----+-----+-----+-----+-----+ 3240
 TGAGGTAGGACTTTCGGTTCCTGCGTCCCTACAGCGACCCCGGTTCCCGCGCGCGCGG
 a T P S * K P R T Q G C R W G P R A P P A -
 b L H P E S Q E R R D V A G G Q G R R R P -
 c S I L K A K N A G M S L G A K G A A G P -
 CTCTGCCCTCCGAGGCGCTGCACTGTGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC
 3241 -----+-----+-----+-----+-----+ 3300
 GAGACGGGAGGCTCCGCGACGTCAACGACACGCTGTGCTAAGGACGAGTTCGACTGAG
 a L C P P R P C S G C A T K H S C S S * L -
 b S A L R G R A V A V P P S I P A Q A D S -
 c L P S E A V Q W L C H Q A P L L K L T R -
 GACACGCTGTCACTAGTGCACCTCTGGGGTCACTCAGGACAGCCGACGACGCTGA
 3301 -----+-----+-----+-----+-----+ 3360
 CTGTGACACAGTGSATGACCGGTGAGGACCCAGTGAGTCTGCTGGGTCTGGGTGAGCT
 a D T V S P T C H S W G H S G Q P R R S * -
 b T P C H L R A T P G V T Q D S P D A A E -
 c H R V T Y V P L L G S L R T A Q T Q L S -
 GTCCGAGCTCCCGGGGACGACGCTGACTGCGCTGGAGCGCGACGCAACCCGACCTGTC
 3361 -----+-----+-----+-----+-----+ 3420
 CAGCCTTCGAGGCGCCCTGCTGCGACTGACGGGACCTCGGCGCTGCTGGGTGGCGCTGAGC

 FIG. 51
 (CONTINUED)

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 a V G S S R G R R * L P W R P Q P T R H C -
 b S E A P G D D A D C P G G R S Q P G T A -
 c R K L P G T T L T A L E A A N P A L P -
 CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGAGAGCA
 3421 -----+-----+-----+-----+ 3480
 GGAGTCTGAAGTCTCTGGTAGGACCTGACTACCGGTGGGCGGGTGTCTGGTCCGGCTCTGGT
 a P Q T S R P S W T D G H P P T A R P R A -
 b L R L Q D H P G L M A T R P Q P G R E Q -
 c S D F K T I L D * W P P A H S Q A E S R -
 GACACAGCAGCCCTGTCAAGCCGGCTCTACGTCCAGGGAGGGAGGGCGGCCACAC
 3481 -----+-----+-----+-----+ 3540
 CTGTGGTCTCTGGGACAGTGGCGCCCGAGATGCAAGGTCCCTCCCTCCCGCCGGGTGTG
 a D T S S P V T P G S T S Q G G R G G P H -
 b T P A A L S R R A L R P R E G G A A H T -
 c H Q Q P C H A G L Y V P G R E G R P T P -
 CCAGCCCGCAGCCGCTGGAGCTGAGGCTGAGTGAGTGTGGCCGAGCGCTGCATGT
 3541 -----+-----+-----+-----+ 3600
 GGTCCGGCGTGGCGACCTCAGACTCCGGACTCACTACAAACCGGCTCCGGAAGTACA
 a P G P H R W E S E A * V S V W P R P A C -
 b Q A R T A G S L R P E * V F G R G L H V -
 c R P A P L G V * G L S E C L A E A C M S -
 CGCGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAGGGCTGAGTG
 3601 -----+-----+-----+-----+ 3660
 GGCAGACTTCCGACTCAGAGGCCGACTCCGACTCGCTCAGGTGGGTCCCGACTCAC
 a P A E G * V S G * G L S E C P A K G * V -
 b R L K A E C P A E A * A S V Q P R A E C -
 c G * R L S V R L R P E R V S S Q G L S V -
 TCCAGCACACTGCGGTCTTCACTTCCCCACAGGCTGGCGCTCCGCTCCACCCAGGGCC
 3661 -----+-----+-----+-----+ 3720
 AGGTCTGTGGACGGCAGAGTGAAGGGGTGTCCGACCGAGCCGAGGTGGGGTCCCGG
 a S S T P A V F T S P Q A G A R L H P R A -
 b P A H L P S S L P H R L A L G S T P G P -
 c Q H T C R L H F P T G W R S A P P G Q G -
 AGCTTTTCTCTCCAGGAGCCCGCTTCCACTCCCAATAGGAATAGTCCATCCCCAGA
 3721 -----+-----+-----+-----+ 3780
 TCGAAAGAGTGGTCTCTGGGCCGAGGTGAGGGGTGTATCTCTTATCAGGTAGGGGTCT
 a S F S S P G A R L P L P T * E * S I P R -
 b A F P H Q E P G F H S P H R N S P S P D -
 c L F L T R S P A S T P H I G I V H P Q I -
 TTGCCATTGTTCACCCCTGCGCCTGCGCTCTTTCCTTCCACCCCAACATCCAGTGG
 3781 -----+-----+-----+-----+ 3840
 AAGCGGTAAACAGTGGGAGCGGGACGGAGGAAACGGAAGTGGGGTGGTGGTCCAC
 a F A I V H P S P C P P L P S T P T I Q V -
 b S P L P T P R P A L L C L P P P P S R P D -
 c R H C S P L A L P S F A F H P H H P G -
 GAGACCCCTGAGAAGGACCTGGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTGCCCTG
 3841 -----+-----+-----+-----+ 3900
 CTCTGGGACTCTTCTGGGACCTCGAGACCTTAAGACCTCACTGGTTCACACAGGGAC

 FIG. 51
 (CONTINUED)

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a E T L R R T L G A L G I W S D Q R C A L -
 b R P * E G P W E L W E F G V T K G V P C -
 c D P E K D P G S S G N L E * P K V C P V -
 TACACAGGCGAGGACCOCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGGGAGGT
 3901 -----+-----+-----+-----+ 3960
 ATGTGTCCGCTCCTGGGACGTGGACCTACCCCCAGGGACACCCAGTTTAAACCCCTCCA
 a Y T G E D P A P G W G S L W V K L G G G -
 b T Q A R T L H L D G G P C G S N W G E V -
 c H R R G P C T W M G V P V G Q I G G R C -
 GCTGTGGGAGTAAATACTGAAATATATGAGTTTTTCAGTTTTGAAAAAAAAAAAAAAAAA
 3961 -----+-----+-----+-----+ 4020
 CGACACCCCTCAITTTATGACTTATATACTCAAAAAGTCAAAACTTTTTTTTTTTTTTTT
 a A V G V K Y * I Y E F F S F E K K K K K -
 b L W E * N T E Y M S F S V L K K K K K K -
 c C G S K I L N I * V F Q F * K K K K K K -
 AAAAAAAAAA
 4021 ----- 4029
 TTTTTTTTT
 a K K K -
 b K K -
 c K K -

FIG. 51
(CONTINUED)

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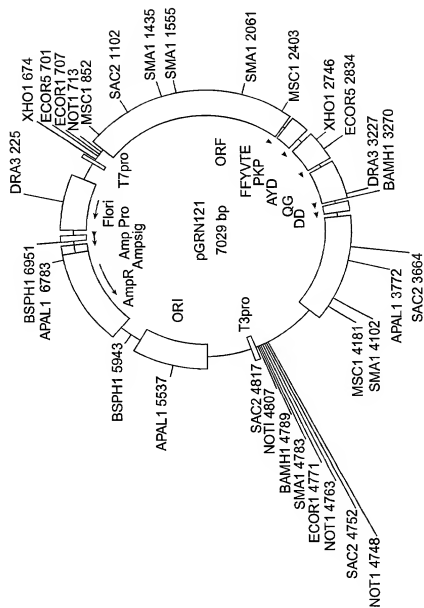


FIG. 52

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1
 met
 GCACGCGCTGCGTCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCG ATG
 10
 pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC
 20
 his tyr arg glu val leu pro leu ala thr phe val arg arg leu
 CAC TAC CGC GAG GTG CTG CCG CTG GCC ACC TTC GTG CGG CGC CTG
 30
 gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
 GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT
 40
 phe arg ala leu val ala gln cys leu val cys val pro trp asp
 TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC
 50
 ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
 GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC
 60
 leu lys glu leu val ala arg val leu gln arg leu cys glu arg
 CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC
 70
 gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
 GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG
 80
 ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
 GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC
 90
 tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
 TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG
 100
 trp gly leu leu leu arg arg val gly asp asp val leu val his
 TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC
 110
 leu leu ala arg cys ala leu phe val leu val ala pro ser cys
 CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC
 120
 ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
 GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GAC
 130
 thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
 ACT CAG GCC CCG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

FIG. 53

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200
 leu gly cys glu arg ala trp asn his ser val arg glu ala gly
 CTG GGA TGC GAA CCG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

210
 val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
 GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CCG GGG GGC

220
 ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
 AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

230
 ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
 GCT GCC CCT GAG CCG GAG CCG ACG CCC GTT GGG CAG GGG TCC TGG

240
 ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
 GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

250
 val val ser pro ala arg pro ala glu ala thr ser leu glu
 GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

260
 gly ala leu ser gly thr arg his ser his pro ser val gly arg
 GGT GCG CTC TCT GGC ACG CCG CAC TCC CAC CCA TCC GTG GGC CCG

270
 gln his his ala gly pro pro ser thr ser arg pro pro arg pro
 CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CCG CCA CCA CGT CCC

280
 trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
 TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

290
 leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
 CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CCG CCC TCC TTC CTA

300
 leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
 CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CCG AGG CTC GTG

310
 glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
 GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

320
 arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
 CGC AGG TTG CCC CCG CTG CCC CAG CCG TAC TGG CAA ATG CCG CCC

330
 leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
 CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

340
 val leu leu lys thr his cys pro leu arg ala ala val thr pro
 GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

350
 360
 370
 380
 390
 400
 410
 420

FIG. 53
(CONTINUED)

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ala ala gly val cys ala arg glu lys pro gln gly ser val ala
 GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

430
 ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
 GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

440
 leu arg gln his ser ser pro trp gln val tyr gly phe val arg
 CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

460
 ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
 GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

470
 his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
 CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

490
 leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
 CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

500
 met ser val arg asp cys ala trp leu arg arg ser pro gly val
 ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

520
 gly cys val pro ala ala glu his arg leu arg glu glu ile leu
 GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

540
 ala lys phe leu his trp leu met ser val tyr val val glu leu
 GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

550
 leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
 CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

560
 arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
 AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

580
 ile gly ile arg gln his leu lys arg val gln leu arg glu leu
 ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

600
 ser glu ala glu val arg gln his arg glu ala arg pro ala leu
 TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

610
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

620
 pro ile val asn met asp tyr val val gly ala arg thr phe arg
 CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

630

FIG. 53
(CONTINUED)

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200405 04100
 200405 04100

650
 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

660
 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
 TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

670
 gly ala ser val leu gly leu asp asp ile his arg ala trp arg
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

680
 thr phe val leu arg val arg ala gln asp pro pro pro glu leu
 ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

690
 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

700
 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

710
 asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
 AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

720
 his gly his val arg lys ala phe lys ser his val ser thr leu
 CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

730
 thr asp leu gln pro tyr met arg gln phe val ala his leu gln
 ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

740
 glu thr ser pro leu arg asp ala val val ile glu gln ser ser
 GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

750
 ser leu asn glu ala ser ser gly leu phe asp val phe leu arg
 TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

760
 phe met cys his his ala val arg ile arg gly lys ser tyr val
 TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

770
 gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu
 CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

780
 cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly
 TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

790
 ile arg arg asp gly leu leu leu arg leu val asp asp phe leu
 ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG

FIG. 53
(CONTINUED)

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880
 leu val thr pro his leu thr his ala lys thr phe leu arg thr
 TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

890
 leu val arg gly val pro glu tyr gly cys val val asn leu arg
 CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

910
 lys thr val val asn phe pro val glu asp glu ala leu gly gly
 AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

920
 thr ala phe val gln met pro ala his gly leu phe pro trp cys
 ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

940
 gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
 GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950
 ser ser tyr ala arg thr ser ile arg ala ser leu thr phe asn
 TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC

970
 arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
 CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980
 val leu arg leu lys cys his ser leu phe leu asp leu gln val
 GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

1000
 asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
 AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010
 leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
 CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030
 his gln gln val trp lys asn pro thr phe phe leu arg val ile
 CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040
 ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
 TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060
 ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
 GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1070
 ser glu ala val gln trp leu cys his gln ala phe leu leu lys
 TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1080
 leu thr arg his arg val thr tyr val pro leu leu gly ser leu
 CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

FIG. 53
(CONTINUED)

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1100
 arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
 AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120
 leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
 CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

1130 1132
 phe lys thr ile leu asp OP
 TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCTGTACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCACACCC
 AGGCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTTTGGCCGAGGCCCTGCATGTCC
 GGCCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGCCAGCCAAGGGCTGAGTGTCTC
 CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCCGCCCTCCACCCACAGGGCCAG
 CTTTTTCYTACCAGGAGCCCGGCTTCACACTCCCCACATAGGAATAGTCCATCCCCAGATT
 CGCCATGTGTTACCCYTCGCCCTGCCYTCCTTTGGCTTCCACCCCCACCATCCAGGTGGA
 GACCCTGAGAAGGACCCCTGGGAGCTCTGGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTGA
 CACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC
 TGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAA

FIG. 53
(CONTINUED)

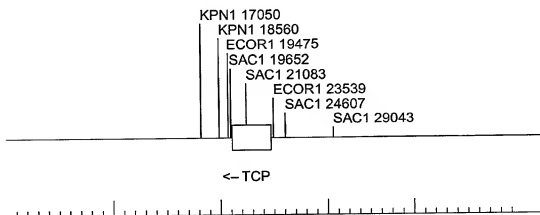


FIG. 54

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